

FIG. 1

1  
GAATTCC GACCGCAGAC

18  
ATG AAA CTT GTC TTC CTC GTC CTG CTG TTC CTC GGG GCC CTC GGA CTC  
met lys leu val phe leu val leu leu phe leu gly ala leu gly leu  
1

66  
TGT CTG GCT GGC CGT AGG AGA AGG AGT GTT CAG TGG TGC ACC GTA TCC  
cys leu ala gly arg arg arg arg ser val gln trp cys thr val ser  
17

114  
CAA CCC GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AGA  
gln pro glu ala thr lys cys phe gln trp gln arg asn met arg arg  
33

162  
GTG CGT GGC CCT CCT GTC AGC TGC ATA AAG AGA GAC TCC CCC ATC CAG  
val arg gly pro pro val ser cys ile lys arg asp ser pro ile gln  
49

210  
TGT ATC CAG GCC ATT GCG GAA AAC AGG GCC GAT GCT GTG ACC CTT GAT  
cys ile gln ala ile ala glu asn arg ala asp ala val thr leu asp  
65

258  
GGT GGT TTC ATA TAC GAG GCA GGC CTG GCC CCC TAC AAA CTC CGA CCT  
gly gly phe ile tyr glu ala gly leu ala pro tyr lys leu arg pro  
81

306  
GTA GCG GCG GAA GTC TAC GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT  
val ala ala glu val tyr gly thr glu arg gln pro arg thr his tyr  
97

354  
TAT GCC GTG GCT GIG GTG AAG AAG GGC GGC AGC TTT CAG CTG AAC GAA  
tyr ala val ala val val lys lys gly gly ser phe gln leu asn glu  
113

402  
CTG CAA GGT CTG AAG TCC TGC CAC ACA GGC CTT CGC AGG ACC GCT GGA  
leu gln gly leu lys ser cys his thr gly leu arg arg thr ala gly  
129

450  
TGG AAT GTG CCT ATA GGG ACA CTT CGT CCA TTC TTG AAT TGG ACG GGT  
trp asn val pro ile gly thr leu arg pro phe leu asn trp thr gly  
145

FIG. 2A

498  
 CCA CCT GAG CCC ATT GAG GCA GCT GTG GCC AGG TTC TTC TCA GCC AGC  
 pro pro glu pro ile glu ala ala val ala-arg phe phe ser ala ser  
 161

546  
 TGT GTT CCC GGT GCA GAT AAA GGA CAG TTC CCC AAC CTG TCT CGC CTG  
 cys val pro gly ala asp lys gly gln phe pro asn leu cys arg leu  
 177

594  
 TGT GCG GGG ACA GGG GAA AAC AAA TGT GCC TTC TCC TCC CAG GAA CCG  
 cys ala gly thr gly glu asn lys cys ala phe ser ser gln glu pro  
 193

642  
 TAC TTC AGC TAC TCT GGT GCC TTC AAG TGT CTG AGA GAC GGG GCT GGA  
 tyr phe ser tyr ser gly ala phe lys cys leu arg asp gly ala gly  
 209

690  
 GAC GTG GCT TTT ATC AGA GAG AGC ACA GTG TTT GAG GAC CTG TCA GAC  
 asp val ala phe ile arg glu ser thr val phe glu asp leu ser asp  
 225

738  
 GAG GCT GAA AGG GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGG  
 glu ala glu arg asp glu tyr glu leu leu cys pro asp asn thr arg  
 241

786  
 AAG CCA GTG GAC AAG TTC AAA GAC TGC CAT CTG GCC CGG GTC CCT TCT  
 lys pro val asp lys phe lys asp cys his leu ala arg val pro ser  
 257

834  
 CAT GCC GTT GTG GCA CGA AGT GTC AAT GGC AAG GAG GAT GCC ATC TGG  
 his ala val val ala arg ser val asn gly lys glu asp ala ile trp  
 273

882  
 AAT CTT CTC CGC CAG GCA CAG GAA AAG TTT GGA AAG GAC AAG TCA CCG  
 asn leu leu arg gln ala gln gln lys phe gly lys asp lys ser pro  
 289

930  
 AAA TTC CAG CTC TTT GGC TCC GCT AGT GGG CAG AAA GAT CTG CTG TTC  
 lys phe gln leu phe gly ser pro ser gly gln lys asp leu leu phe  
 305

978  
 AAG GAC TCT GCC ATT GGG TTT TCG AGG CTG CCC CCG AGG ATA GAT TCT  
 lys asp ser ala ile gly phe ser arg val pro pro arg ile asp ser  
 321

1026  
 GGG CTG TAC CTT GGC TCC GCC TAC TTC ACT GCC ATC CAG AAC TTG AGG  
 gly leu tyr leu gly ser gly tyr phe thr ala ile gln asn leu arg  
 337

FIG. 2B

1074  
 AAA AGT GAG GAG GAA GTG GCT GCC CGG CGT GCG CGG GTC GTG TGG TGT  
 lys ser glu glu glu val ala ala arg arg ala arg val val trp cys  
 353  
 1122  
 GCG GTG GGC GAG CAG GAG CTG CGC AAG TGT AAC CAG TGG AGT GGC TTG  
 ala val gly glu gln glu leu arg lys cys asn gln trp ser gly leu  
 369  
 1170  
 AGC GAA GGC AGC GTG ACC TGC TCC TCG GCC TCC ACC ACA GAG GAC TGC  
 ser glu gly ser val thr cys ser ser ala ser thr thr glu asp cys  
 385  
 1218  
 ATC GCC CTG GTG CTG AAA GGA GAA GCT GAT GCC ATG AGT TTG GAT GGA  
 ile ala leu val leu lys gly glu ala asp ala met ser leu asp gly  
 401  
 1266  
 GGA TAT GTG TAC ACT GCA GGC AAA TGT GGT TTG GTG CCT GTC CTG GCA  
 gly tyr val tyr thr ala gly lys cys gly leu val pro val leu ala  
 417  
 1314  
 GAG AAC TAC AAA TCC CAA CAA AGC AGT GAC CCT GAT CCT AAC TGT GTG  
 glu asn tyr lys ser gln gln ser ser asp pro asp pro asn cys val  
 433  
 1362  
 GAT AGA CCT GTG GAA GGA TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA  
 asp arg pro val glu gly tyr leu ala val ala val val arg arg ser  
 449  
 1410  
 GAC ACT AGC CTT ACC TGG AAC TCT GTG AAA GGC AAG AAG TCC TGC CAC  
 asp thr ser leu thr trp asn ser val lys gly lys lys ser cys his  
 465  
 1458  
 ACC GCC GTG GAC AGG ACT GCA GGC TGG AAT ATC CCC ATG GGC CTG CTC  
 thr ala val asp arg thr ala gly trp asn ile pro met gly leu leu  
 481  
 1506  
 TTC AAC CAG ACG GGC TCC TGC AAA TTT GAT GAA TAT TTC AGT CAA AGC  
 phe asn gln thr gly ser cys lys phe asp glu tyr phe ser gln ser  
 497  
 1554  
 TGT GCC CCT GGG TCT GAC CCG AGA TCT AAT CTC TGT GCT CTG TGT ATT  
 cys ala pro gly ser asp pro arg ser asn leu cys ala leu cys ile  
 513  
 1602  
 GGC GAC GAG CAG GGT GAG AAT AAG TGC GTG CCC AAC AGC AAT GAG AGA  
 gly asp glu gln gly glu asn lys cys val pro asn ser asn glu arg  
 529

FIG. 2C

1650  
TAC TAC GGC TAC ACT GGG GCT TTC CGG TGC CTG GCT GAG AAT GCT GGA  
tyr tyr gly tyr thr gly ala phe arg cys leu ala glu asn ala gly  
545

1698  
GAC GTT GCA TTT GTG AAA GAT GTC ACT GTC TTG CAG AAC ACT GAT GGA  
asp val ala phe val lys asp val thr val leu gln asn thr asp gly  
561

1746  
AAT AAC AAT GAG GCA TGG GCT AAG GAT TTG AAG CTG GCA GAC TTT GCG  
asn asn asn glu ala trp ala lys asp leu lys leu ala asp phe ala  
577

1794  
CTG CTG TGC CTC GAT GGC AAA CGG AAG CCT GTG ACT GAG GCT AGA AGC  
leu leu cys leu asp gly lys arg lys pro val thr glu ala arg ser  
593

1842  
TSC CAT CTT GCC ATG GCC CCG AAT CAT GCC GTG GTG TCT CGG ATG GAT  
cys his leu ala met ala pro asn his ala val val ser arg met asp  
609

1890  
AAG GTG GAA CGC CTG AAA CAG GTG CTG CTC CAC CAA CAG GCT AAA TTT  
lys val glu arg leu lys gln val leu leu his gln gln ala lys phe  
625

1938  
GGG AGA AAT GGA TCT GAC TGC CCG GAC AAG TTT TGC TTA TTC CAG TCT  
gly arg asn gly ser asp cys pro asp lys phe cys leu phe gln ser  
641

1986  
GAA ACC AAA AAC CTT CTG TTC AAT GAC AAC ACT GAG TGT CTG GCC AGA  
glu thr lys asn leu leu phe asn asp asn thr glu cys leu ala arg  
657

2034  
CTC CAT GGC AAA ACA ACA TAT GAA AAA TAT TTG GGA CCA CAG TAT GTC  
leu his gly lys thr thr tyr glu lys tyr leu gly pro gln tyr val  
673

2082  
GCA GGC ATT ACT AAT CTG AAA AAG TGC TCA ACC TCC CCC CTC CTG GAA  
ala gly ile thr asn leu lys lys cys ser thr ser pro leu leu glu  
689

2130  
GCC TGT GAA TTC CTC AGG AAG TAA  
ala cys glu phe leu arg lys \*\*\* ACCGAA GAAGATGGCC CAGCTCCCCA  
705

2180  
AGAAAGCCTC AGCCATTAC TGCCCCCAGC TCTTCTCCCC AGGTGTGTIG GGGCCTTGCC

2240  
TCCCCTGCTG AAGGTGGGA TTGCCCATCC ATCTGCTTAC AATTCCCTGC TGTCGTCTTA

2300  
GCAAGAAGTA AAATGAGAAA TTTTGTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

FIG. 2D

MEDIUM	CELL LYSATES
CONTROL	



FIG. 3

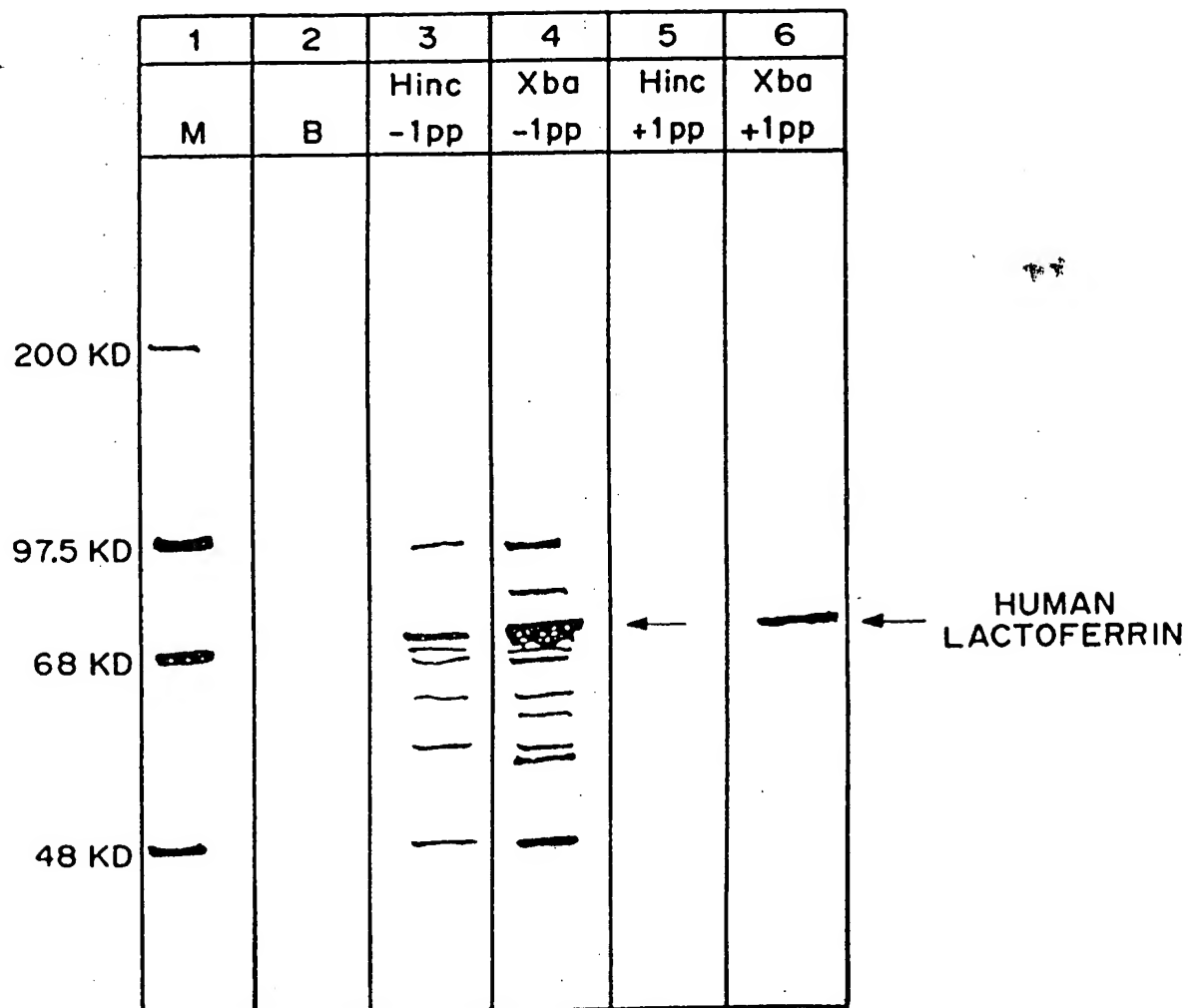


FIG.4

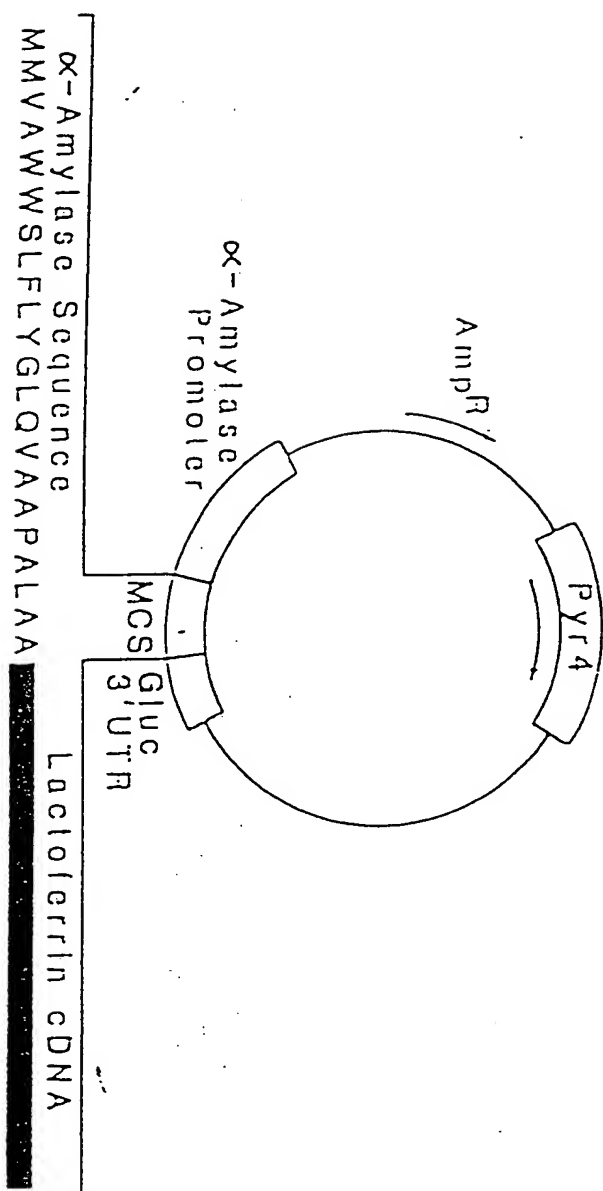


FIG. 5



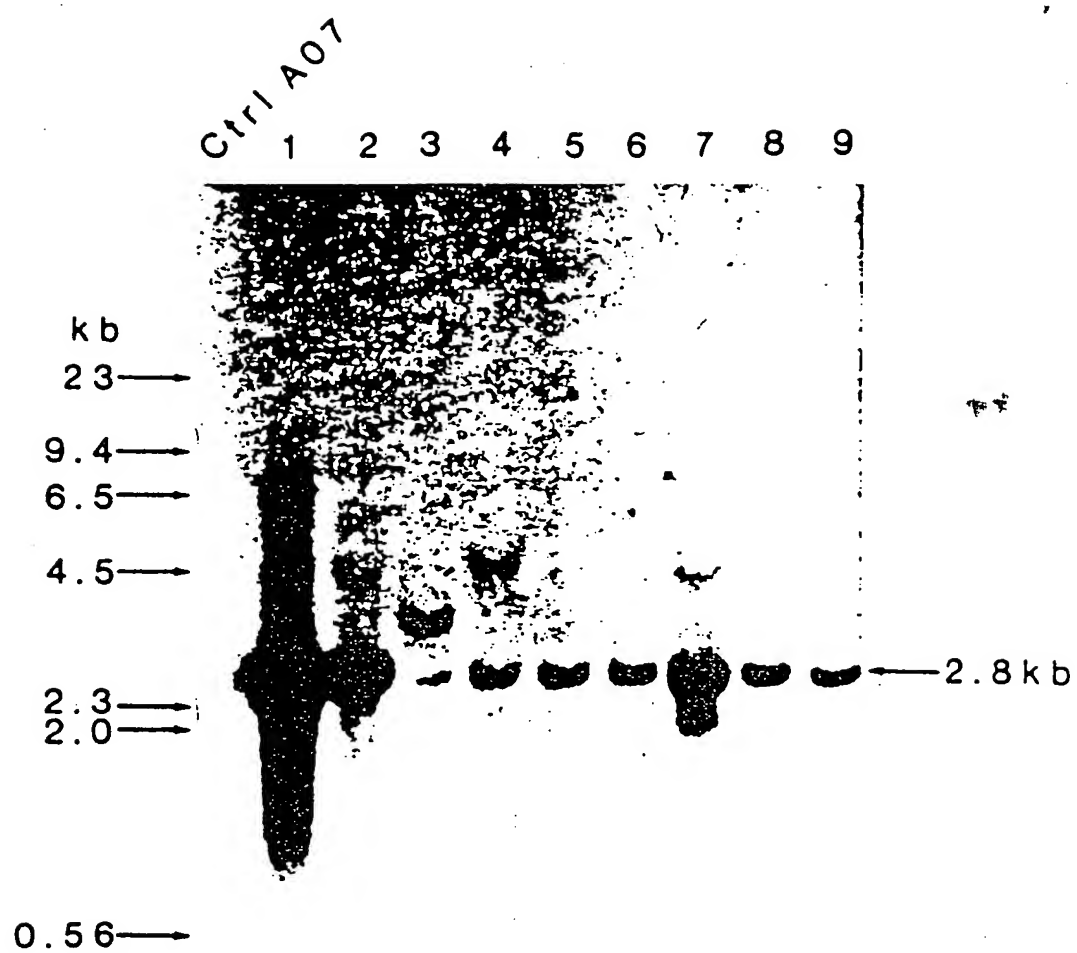


FIG.6

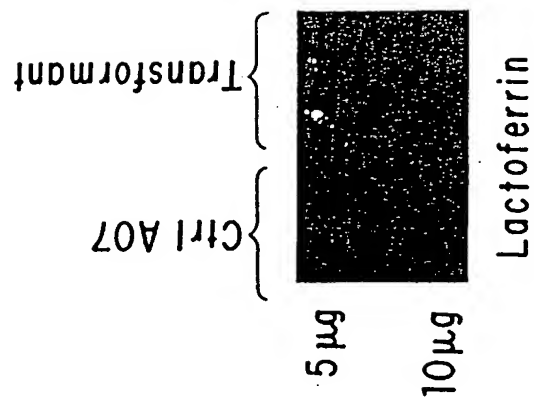
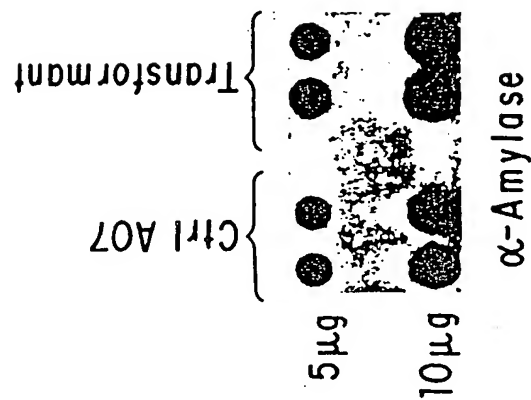
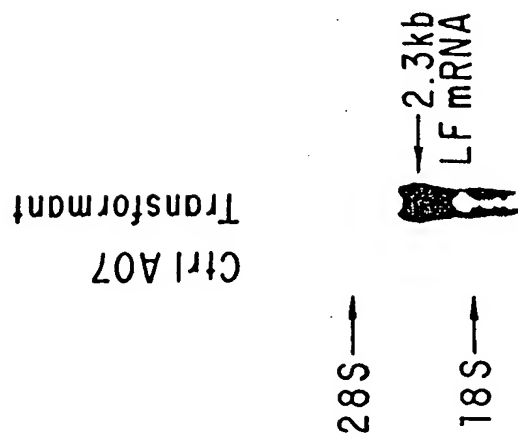


FIG.7A

FIG.7B

FIG.7C

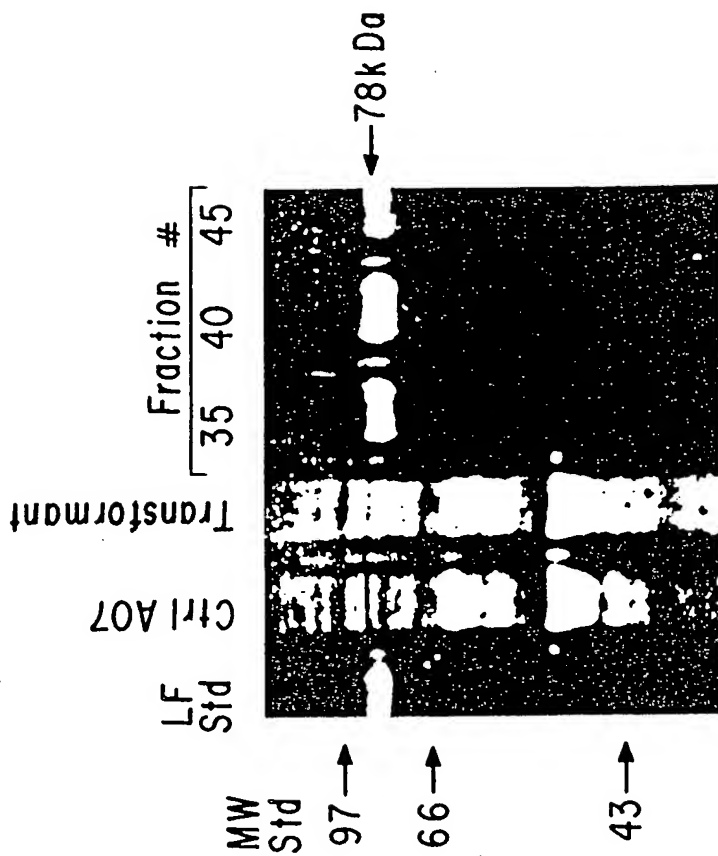


FIG.8B



FIG.8A

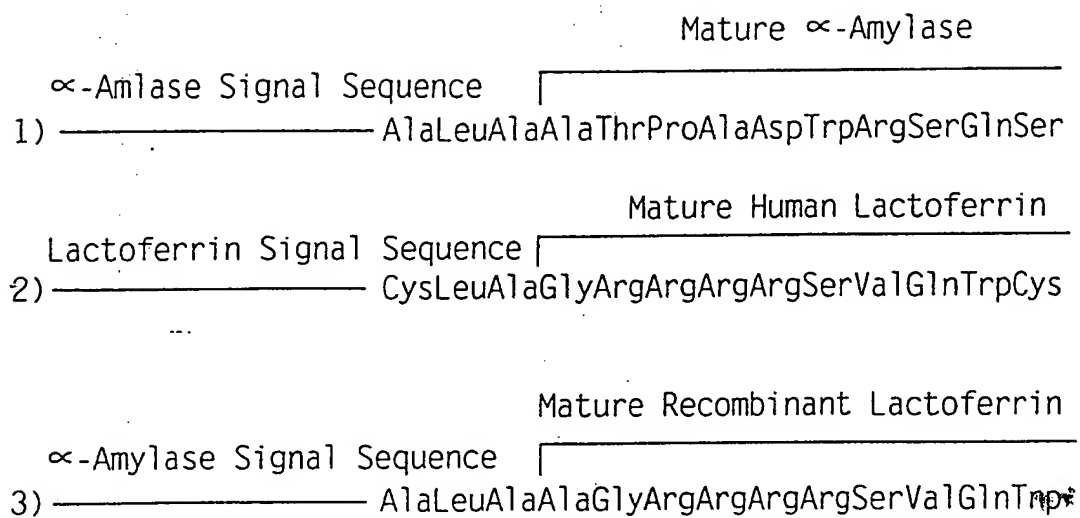


FIG. 8C

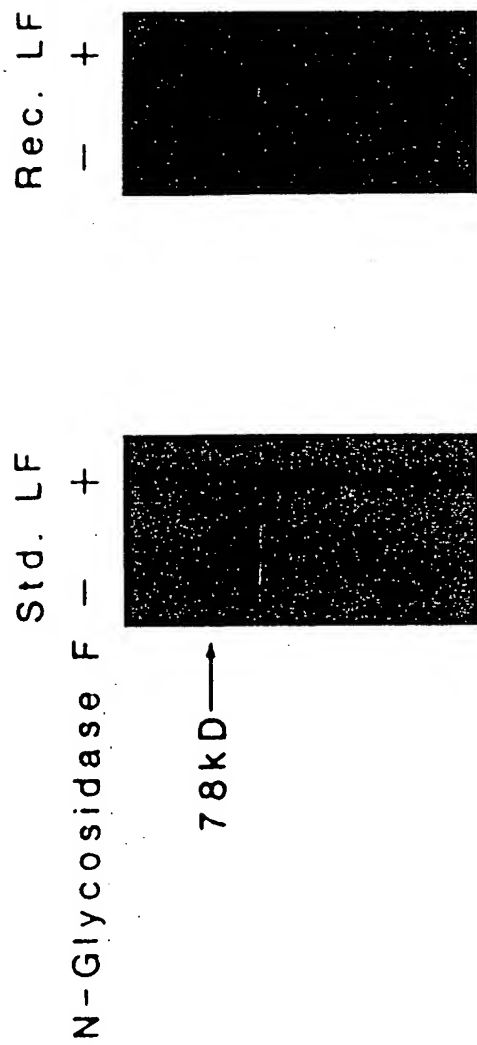


FIG.9A

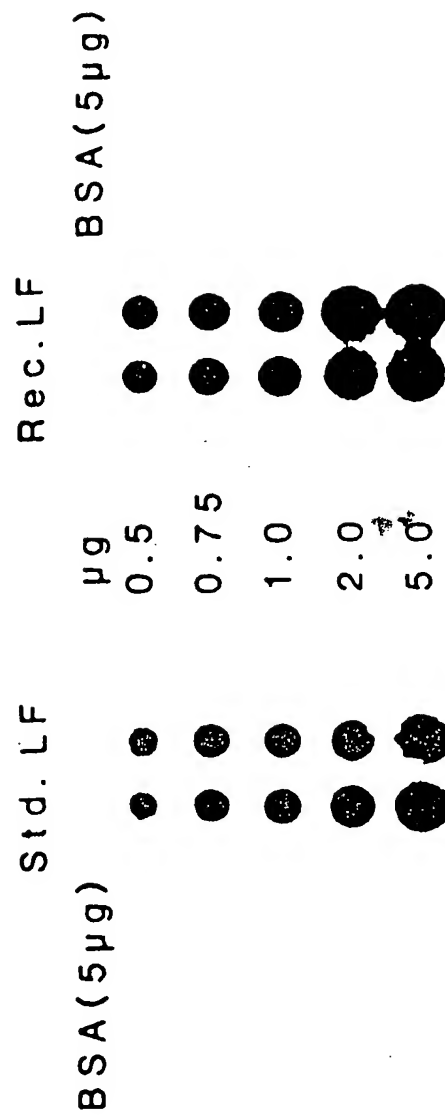


FIG.9B

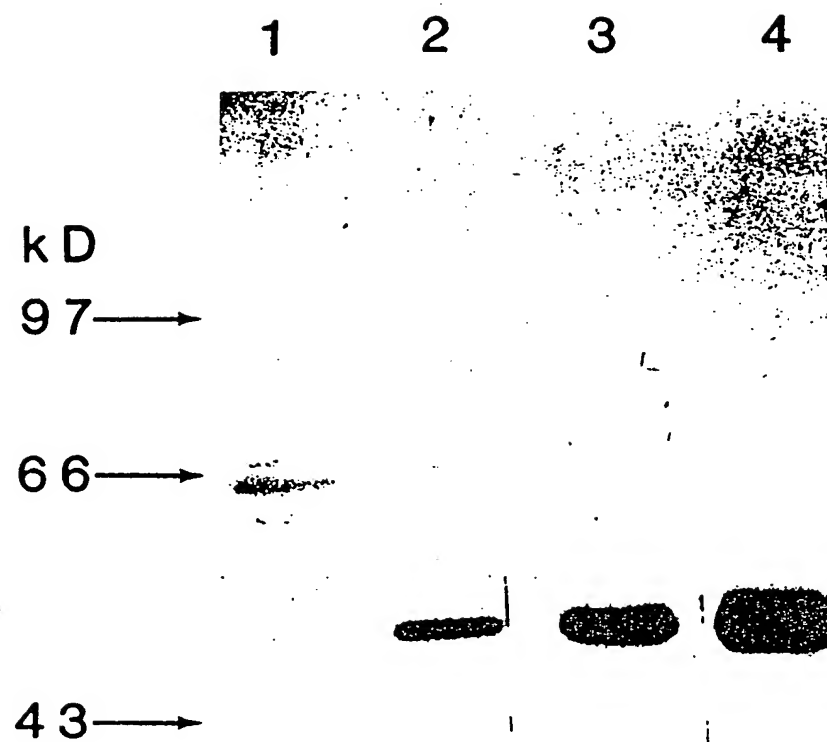


FIG.10

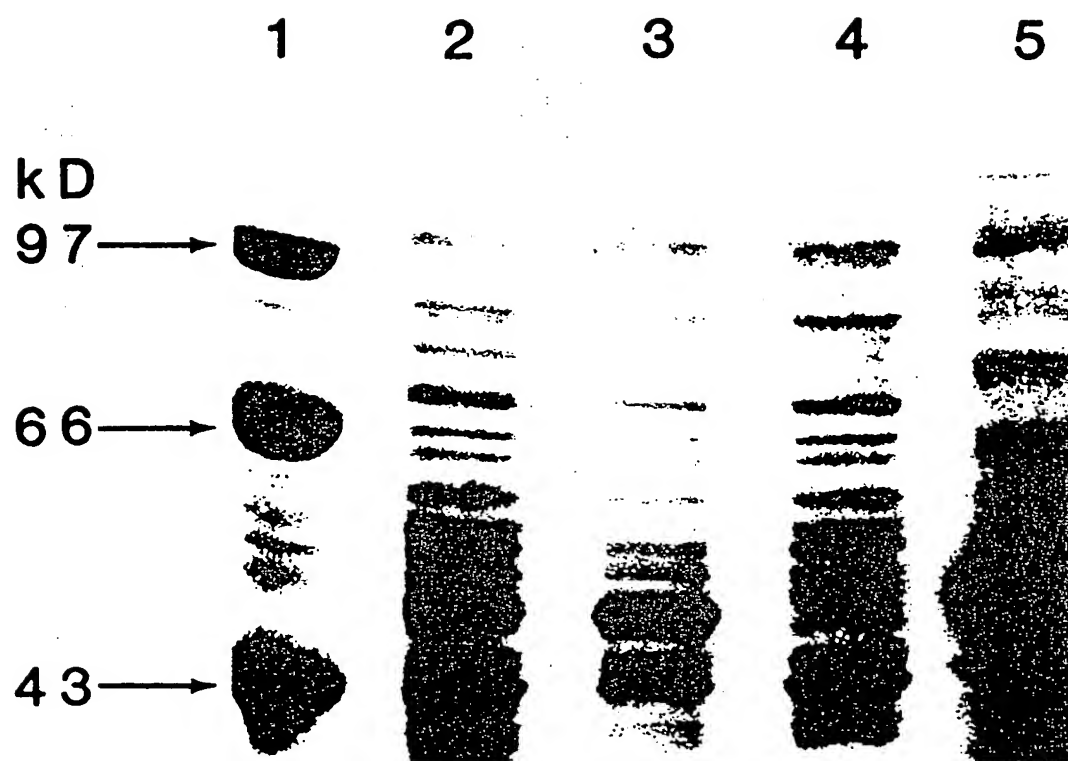


FIG.11

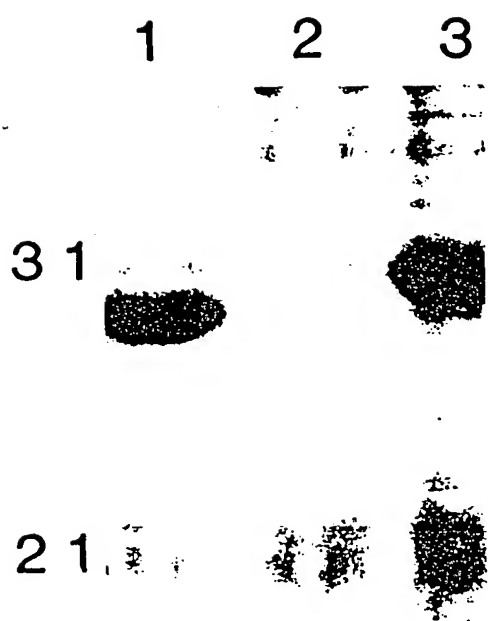


FIG.12A

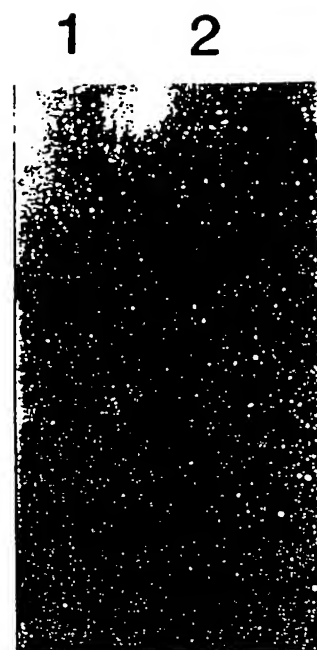


FIG.12B



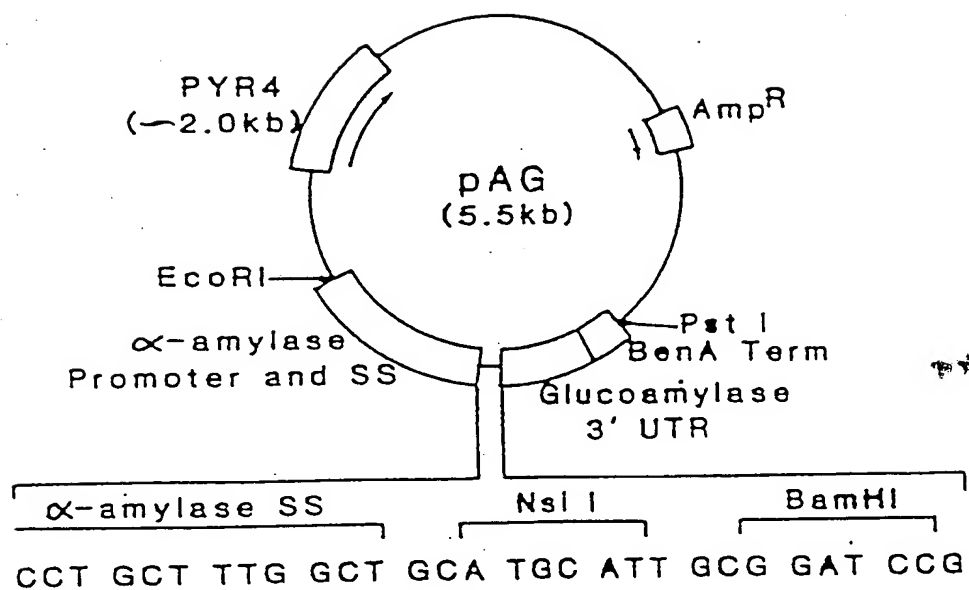


FIG. 13

1 NNNNGAGCCT TCGTTCGGGA GTGCCCCAG GACGCCAGCC CATGAAGCTC  
51 TTCGTCCCCG CCTCCTGTC CCTTGGAGCC CTGGACTGT GTCTGGCTGC  
101 CCCGAGGAAA AACGTTGAT GGTGTACCAT CTCCCAACCT GAGTGGTTCA  
151 AATGCCGCAG ATGSCAGTGG AGGATGAAGA AGCTGGGTGC TCCCTCTATC  
201 ACCTGTGTGA GCGGGGCCCTT TGCCTTGGA TGTATTCCGG GCATCGCGGA  
251 GAAAAAGGCG GATGCTGTGA CCCTGGATGG TGGCATGCTG TTTGAGGCGG  
301 GCCGGGACCC CTACAACTG CGSCCAGTAG CAGCAGAGAT CTATGGGACC  
351 AAAGAGTCTC CCCAAACCCA CTATTATGCT GTGGCCGTGG TGAAGAAGSG  
401 CAGCAACTTT CAGCTGGACC AGCTGCAAGG CCGGAAGTCC TCCCATACGG  
451 GCCTTGGCAG GTCCGCTGGG TGGATCATCC CTATGGGAAT CCTTGGCCCC  
501 TACTTGAGCT GGACAGAGTC ACTCGAGCCC CTCCAGGGAG CTGTGGCTAA  
551 ATTCTTCTCT GCCAGCTGTG TTCCCTGCAT TGATAGACAA CCATACCCCA  
601 ACCTGTGTCA ACTGTGCAAG GGGGAGGGGG AGAACCAGTG TGCCTGCTCC  
651 TCCCGGGAAC CATACTTCGG TTATTCTGCT GCCTTCAAGT GTCTGCAGGA  
701 CGGGGCTGGA GACGTGSCCT TTGTTAAAGA GACGACAGTG TTTGAGAAGT  
751 TGCCAGAGAA GGCTGACAGG GACCAGTATG AGCTTCTCTG CCTGAACAAC  
801 AGTCGGGCGC CAGTGGATGC GTTCAAGGAG TCCACCTGG CCCAGGTCCC  
851 TTCTCATGCT GTCGTGGCCC GAAGTGTGGA TGGCAAGGAA GACTTGATCT  
901 GGAAGCTTCT CAGCAAGGCG CAGGAGAAAT CTGGAAGAAA CAAGTCTCGG  
951 AGCTTCCAGC TCTTTGGCTC TCCACCCGGC CAGAGGGACC TGCTGTTCAA  
1001 AGACTCTGCT CTTGGGTTTT TGAGGATCCC CTCGAAGSTA GATTGGCGGC  
1051 TGTACCTGGG CTCCCGCTAC TTGACCACCT TGAAGAACCT CAGGGAAACT  
1101 GCGGAGGAGG TGAAGGCGCG GTACACCAGG STCGTGTGCT GTGCCGTGGG  
1151 ACCTGAGGAG CAGAAGAAGT GCCAGCAGTG GAGCCAGCAG AGCGGCCAGA  
1201 ACGTGACCTG TCCACGCGCG TCCACCACTG ACQACTGCAT CGTCTGGTG  
1251 CTGAAAGGGG AAGCAGATGC CCTGAACCTG GATCGAGGAT ATATCTACAC  
1301 TCGGGGCAAG TGTGGCCTGG TGCCTGTCTT GGCAGAGAAC CGGAAATCCT  
1351 CCAAACACAG TAGCCTAGAT TGTGTGCTGA GACCAACGGA AGGGTACCTT  
1401 GCCGTGGCAG TTGTCAAGAA AGCAAATGAG GGGCTCACAT GGAATTCTCT

FIG. 14A

1451 GAAAGACAAG AAGTCGTGCC ACACCGCCGT GGACAGGACT GCAGGCTGGA  
1501 ACATCCCCAT GGGCCTGATC GTCAACCAGA CAGGCTCCTG CGCATTTGAT  
1551 GAATTCTTTA GTCAGAGCTG TGCCCCTGGG GCTGACCCGA AATCCAGACT  
1601 CTGTGCCTTG TGTGCTGGCG ATGACCAGGG CCTGGACAAG TGTGTGCCCCA  
1651 ACTCTAAGGA GAAGTACTAT GGCTATACCG GGGCTTTCAG GTGCCTGGCT  
1701 GAGGACGTTG GGGACGTTGC CTTTGTGAAA AACGACACAG TCTGGGAGAA  
1751 CACGAATGGA GAGAGCACTG CAGACTGGGC TAAGAACTTG AATCGTGAGG  
1801 ACTTCAGGTT GCTCTGCCTC GATGGCACCA GGAAGCCTGT GACGGAGGCT  
1851 CAGAGCTGCC ACCTGGCGGT GGCCCCGAAT CACGCTGTGG TGTCTCGGAG  
1901 CGATAGGGCA GCACACGTGA AACAGGTGCT GCTCCACCAG CAGGCTCTGT  
1951 TTGGGAAAAA TGGAAAAAAC TGCCCGGACA AGTTTTGTTT GTTCAAATCT  
2001 GAAACCAAAA ACCTTCTGTT CAATGACAAC ACTGAGTGTC TGGCCAAACT  
2051 TGGAGGCAGA CCAACGTATG AAGAATATTT GGGGACAGAG TATGTCACGG  
2101 CCATTGCCAA CCTGAAAAAA TGCTCAACCT CCCCCTTCT GGAAGCCTGC  
2151 GCCTTCCTGA CGAGGTAAAG CCTGCAAAGA AGCTAGCCTG CCTCCCTGGG  
2201 CCTCAGCTCC TCCCTGCTCT CAGCCCCAAT CTCCAGGCGC GAGGGACCTT  
2251 CCTCTCCCTT CCTGAAGTCG GATTTTTGCC AAGCTCATCA GTATTTACAA  
2301 TTCCCTGCTG TCATTTTAGC AAGAAATAAA ATTAGAAATG CTGTTGAAAA  
2351 A

FIG. 14B

MKLFVPALLSLGALGLCLAAPRKNNRWCTISQPEWFKCRRWQWRMKKLGAPSIITCVRRAFAL  
ECIPGIAEKKADAVTLTGGMVFEAGRDPYKLRPVAAEIIYGTKEPQTHYYAVAVVKKGSNFQ  
LDQLQGRKSCHTGLGRSAGWIIIPMGILRPYLSWTESLEPLQGAVAKFFSASCVP CIDROAYP  
NLCQLCKGEGENQCACSSREPYFGYSGAFKCLQDGAGDVAFVKETTTFENLPEKADRDQYEL  
LCLNNSRAPVDAFKECHLAQVP SHAVVARSV DGEDLIWKLLSKAQEKSGKNKSRSFQLFGS  
PPGQRDLLFKDSALGFLRIPSKVDSALYLGSRYLTTLKNLRETAEVVKARYTRVVWCAVGPE  
EQKKCQWSQQSGQNVTCATASTTDDCIVLVKGEADALNLDGGYIYTAGKCGLVPVLAENR  
KSSKHSSLDVLRPTEGYLAVAVVKKANEGLTWNLSLXDKKSCHTAVDRTAGWNIIPMGLIVNQ  
TGSCAFDEFFSQSCAPGADPKSRLCALCAGDDQGLDKCVPNSKEKYGYTGAFRCLAEDVGD  
VAFVKNDTVWENTNGESTADWAKNLNREDFRLCLDGTRKPVTEAQSCHLAVAPNHAVVSRS  
DRAAHVKQVLLHQALFGKNGKNCPDKFCLFKSETKNLLFNDNTECLAKLGRPTYEYVLT  
EYVTAIANLKKCSTSPLEACAFLTR

FIG. 14C

1 ACATGAAGCT CTTTCATCCCC GCCCTGCTGT TCCTCGGGAC ACTTGGACTG  
51 TGTCTGGCTG CCCCTAAGAA AGGGGTTTGA TGGTGTGTCA TATCCACAGC  
101 AGAGTATTCA AAATGCCGCC AGTGGCAATC AAAGATAAGA AGAACTAATC  
151 CCATGTTCTG CATAAGGAGG GCTTCTCCCA CTGACTGTAT CCGGGCCATC  
201 GCGGCAAAAA GGGCAGATGC TGTGACCCTT GATGGTGGTT TGGTGTTTGA  
251 AGCAGACCAG TACAACTGC GGCCGGTAGC AGCGGAGATC TACGGGACAG  
301 AAGAGAATCC CCAAACCTAC TATTATGCTG TGGCTGTAGT GAAGAAAGGT  
331 TTCAACTTTC AGAACCAGCT ACAAGGTGGA AAGTCCTGCC ACACAGGCCCT  
401 TGGCAGGTCT GCGGGGTGGA ATATCCCTAT AGGGTTACTT CCGCGTTTCT  
451 TGGACTGGGC AGGGCCACCT GAGCCCTCC AGAAAGCTGT GSCCAAATTC  
501 TTCTCTCAGA GCTGTGTGCC CTGCGCAGAT GGAATGCGT ATCCCAACCT  
551 GTGTCAGCTG TGCATAGGGA AAGSGAAGA TAAATGTGCT TGTTCCTCCC  
601 AGGAACCGTA TTTTGGCTAT TCCGCTGCCT TCAACTGTCT GCACAAAGGG  
651 ATTGGAGATG TGGCTTTTGT CAAGGAGAGT ACAGTGTTC AGAACCTGCC  
701 ACAGAAGGCT GACCGGGACA AATACGAGCT ACTCTGCCCC GACAATACTC  
751 GAAAGCCAGT GGAAGCATTG AGGGAGTCCC ACCTTGCCCC GGTCCCTTCT  
801 CATGCTGTTG TGSCCCGAAG TGTGAATGGC AAGGAGAACT CCATCTGGGA  
851 GCTTCTCTAC CAGTCACAGA AAAAGTTTGG AAAAAGCAAT CCACAGGAGT  
901 TCCAGCTCTT TGGCTCTCCT GGTGAGCAGA AGGACCTCCT GTTTAGAGAT  
951 GCTACCATCG GGTTTTTTGA GATCCCCCTCA AAGATAGATT CTAAGCTGTA  
1001 CCTGGGCCCTC CCGTACCTTA CTGCCATCCA GGGCCTGAGG GAAACGGCAG  
1051 CGGAGGTGGA GCGCGGGCAG GCGAAGSTCG TGTGGTGGC CGTGGGTCCA  
1101 GAGGAGCTGC GCAAGTGCCG GCASTGGAGC AGCCAGAGCA GCCAGAACCT  
1151 GAACTGCAGC CTGGCCTCCA CCACCGAGGA CTGCATCGTC CAGGTGCTGA  
1201 AAGGAGAAGC TGATGCTATG AGCTTGGATG GAGGATTTAT CTACACTGCC  
1251 GGCAAGTGTG GTTTGCTGCC TGTCTGGCA GAGAACCAA AATCTGCCCA  
1301 AAGCAGTAGC TCAGACTGTG TGCATAGACC AACACAAGGG TATTTGCCG  
1351 TGGCGGTTGT CAGGAAAGCA AATGGTGGTA TCACCTGGAA CTCTGTGAGA  
1401 GGCACGAAGT CCTGCCACAC TGCTGTGGAC AGGACAGCAG GCTGGAAACAT

FIG. 15A

1451 CCCCATGGGC CTGCTTGTCA ACCAGACAGG CTCCTGCAAA TTTGACGAAT  
1501 TCTTTAGTCA AAGCTGTGCT CCTGGGTCTC AGCCGGGATC CAATCTCTGT  
1551 GCACTGTGTG TTGGCAATGA CCAGGGCGTG GACAAGTGTG TGCCCAACAG  
1601 TAATGAGAGA TACTATGGTT ACACCGGGGC TTTCAGGTGC CTGGCTGAGA  
1651 ATGCTGGGGA TGTGGCGTTT GTGAAAGATG TCACTGTCTT GGACARCACC  
1701 AATGGACAGA ACACAGAAGA GTGGGCCAGG GAATTGAGGT CAGATGACTT  
1751 TGAGCTGCTG TGCCTTGATG GCACCAGGAA GCCTGTGACT GAGGCTCAGA  
1801 ACTGTCACCT GGCTGTGGCC CCCAGTCATG CTGTGCTCTC TCGGAAGGAA  
1851 AAGGCAGCAC AGGTGGAACA GGTGCTACTC ACTGACCAGG CTCAGTTTGG  
1901 AAGATACGGA AAAGACTGCC CGGACAAGTT TTGCTTGTTC CGGTCTGAGA  
1951 CCAAAAACCT TCTGTTCAAC GACAACACGG AGGTTCCTGG CCAACTCCAA  
2001 GGCAAAACAA CATACGAAAA ATATTTGGGA TCAGASTATG TCACAGCCAT  
2051 CGCTAACCTG AAACAGTGCT CAGTCTCCCC GCTTCTGGAA GCCTGTGCCT  
2101 TCATGATGAG GTAAAACCGG AAAAGAAGCT GCCCGCCTCC CCAGGGGGCCT  
2151 CAGCTTTCCC TCCTCCCGTC TTGATTCCCA GCTGCCCTGG GCCTGCCTCT  
2201 CTCCCTTCCT GAGGGCAGAC TTTGTTGAGC TCATCCGTTT TCACAATTCC  
2251 CTCGTGCCG

FIG. 15B

1

2

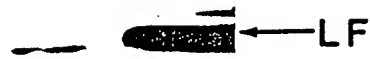


FIG.16

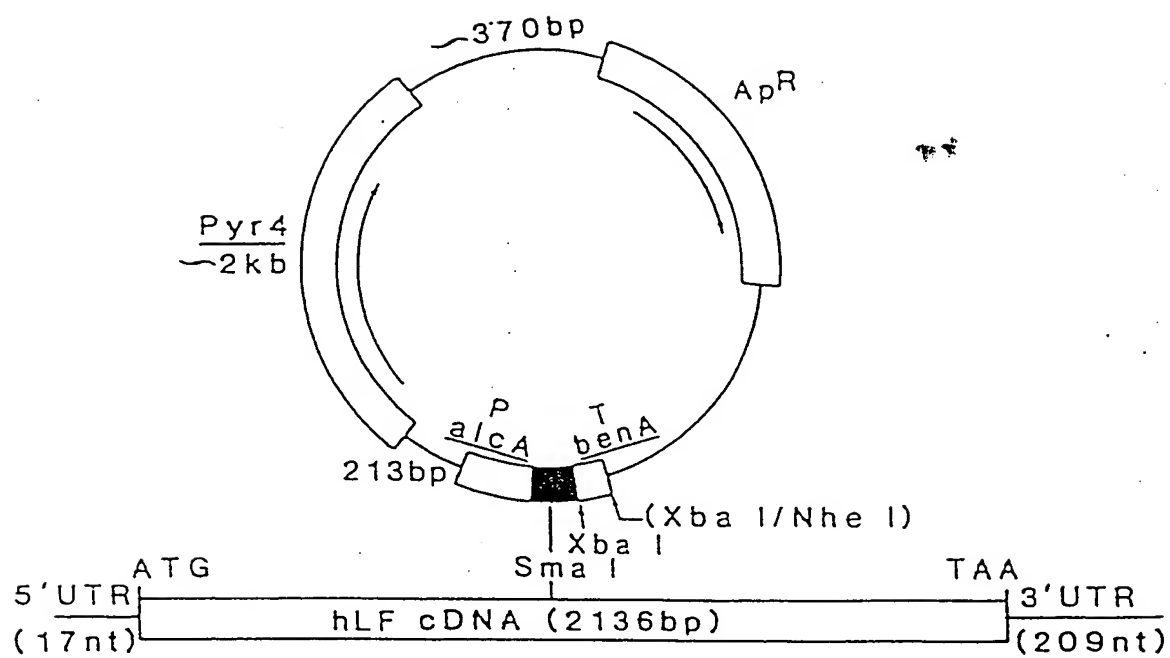


FIG. 17



(Linear) MAPSORT of: hlf2 check: 7473 from: 1 to: 2360  
Mismatch: 0 MinCuts = 1 MaxCuts: 10

AccI GT'mk\_AC

Cuts at: 0 319 2360

Size: 319 2041

AceIII CAGCTCnnnnnnnn'nnnn

Cuts at: 0 948 1125 2183 2219 2360

Size: 948 177 1058 36 141

Fragments arranged by size:

1058 948 177 141 36

AhdI GACnn\_n'nnGTC

Cuts at: 0 472 2360

Size: 472 1888

AlwI GGATCnnnn'n

Cuts at: 0 1341 1955 2360

Size: 1341 614 405

Fragments arranged by size:

1341 614 405

AlwNI CAG\_nnn'CTG

Cuts at: 0 1139 1913 2360

Size: 1139 774 447

Fragments arranged by size:

1139 774 447

ApaI G\_GGCC'C

Cuts at: 0 56 2360

Size: 56 2304

ApaBI GCA\_nnnnn'TGC

Cuts at: 0 1140 1789 2360

Size: 1140 649 571

Fragments arranged by size:

1140 649 571

ApaLI G'TGCA\_C

Cuts at: 0 101 2360

Size: 101 2259

ApoI r'AATT\_y

Cuts at: 0 1 930 1527 1932 2136 2318 2360

Size: 1 929 597 405 204 182 42

Fragments arranged by size:

929 597 405 204 182 42 1

FIG. 18A

AvaI C'yCGr\_G  
Cuts at: 0 48 117 820 1010 1571 2360  
Size: 48 69 703 190 561 789  
Fragments arranged by size:  
789 703 561 190 69 48

AvaII G'GwC\_C  
Cuts at: 0 325 439 495 725 824 2067 2360  
Size: 325 114 56 230 99 1243 293  
Fragments arranged by size:  
1243 325 293 230 114 99 56

BanI G'GyrC\_C  
Cuts at: 0 657 1004 1298 1675 2360  
Size: 657 347 294 377 685  
Fragments arranged by size:  
685 657 377 347 294

BanII G\_rGCy'C  
Cuts at: 0 56 508 1521 2360  
Size: 56 452 1013 839  
Fragments arranged by size:  
1013 839 452 56

BbsI GAAGACnn'nnnn\_  
Cuts at: 0 20 2360  
Size: 20 2340

BbvI GCAGCnnnnnnnn'nnnn\_  
Cuts at: 0 168 394 528 1079 1126 1189 1780 1827  
Size: 168 226 134 551 47 63 591 47  
Cuts at: 1827 1900 2360  
Size: 73 460  
Fragments arranged by size:  
591 551 460 226 168 134 73 63 47 47

Bce83I CTTGAGnnnnnnnnnnnnnn'\_nn'  
Cuts at: 0 1088 1187 2360  
Size: 1088 99 1173  
Fragments arranged by size:  
1173 1088 99

BceII ACGGCnnnnnnnnnnnn'\_n\_  
Cuts at: 0 62 343 823 1447 1670 1855 2360  
Size: 62 281 480 624 223 185 505  
Fragments arranged by size:  
624 505 480 281 223 185 62

FIG. 18B

BfaI C'TA\_G  
 Cuts at: 0 952 1414 1834 2360  
 Size: 952 462 420 526  
 Fragments arranged by size:  
 952 526 462 420

BfiI ACTGGG  
 Cuts at: 0 1664 2360  
 Size: 1664 696

BglI GCCn\_nnn'nGGC  
 Cuts at: 0 427 843 1807 2360  
 Size: 427 416 964 553  
 Fragments arranged by size:  
 964 553 427 416

BglII A'GATC\_T  
 Cuts at: 0 965 1575 2360  
 Size: 965 610 785  
 Fragments arranged by size:  
 965 785 610

BmgI GkGCCC  
 Cuts at: 0 54 1007 1557 1631 2360  
 Size: 54 953 550 74 729  
 Fragments arranged by size:  
 953 729 550 74 54

BpmI CTGGAGnnnnnnnnnnnnnnn\_nn'  
 Cuts at: 0 706 1714 2360  
 Size: 706 1008 646  
 Fragments arranged by size:  
 1008 706 646

Bpu10I CC'TnA\_GC  
 Cuts at: 0 502 1765 2188 2360  
 Size: 502 1263 423 172  
 Fragments arranged by size:  
 1263 502 423 172

BsaWI w'CCGG\_w  
 Cuts at: 0 1672 2360  
 Size: 1672 688

BsaXI ACnnnnnCTCC  
 Cuts at: 0 87 1037 1268 2360  
 Size: 87 950 231 1092  
 Fragments arranged by size:  
 1092 950 231 87

FIG. 18C

BsbI CAACAC  
 Cuts at: 0 778 2014 2227 2360  
 Size: 778 1236 213 133  
 Fragments arranged by size:  
 1236 778 213 133

BscGI CCCGT  
 Cuts at: 0 324 494 681 1517 2360  
 Size: 324 170 187 836 843  
 Fragments arranged by size:  
 843 836 324 187 170

BseRI GAGGAGnnnnnnnnn\_nn'  
 Cuts at: 0 617 1095 1181 2360  
 Size: 617 478 86 1179  
 Fragments arranged by size:  
 1179 617 478 86

BsgI GTGCAGnnnnnnnnnnnnnnn\_nn'  
 Cuts at: 0 577 2360  
 Size: 577 1783

BsiEI CG\_ry'CG  
 Cuts at: 0 10 2360  
 Size: 10 2350

BsiHKA I G\_wGCw'C  
 Cuts at: 0 105 714 1592 2109 2360  
 Size: 105 609 878 517 251  
 Fragments arranged by size:  
 878 609 517 251 105

BsmI GAATG\_Cn'  
 Cuts at: 0 1694 2360  
 Size: 1694 666

BsmAI GTCTCn'nnnn\_  
 Cuts at: 0 187 670 682 1690 1882 2360  
 Size: 187 483 12 1008 192 478  
 Fragments arranged by size:  
 1008 483 478 192 187 12

BsmBI CGTCTCn'nnnn\_  
 Cuts at: 0 670 682 1690 2360  
 Size: 670 12 1008 670  
 Fragments arranged by size:  
 1008 670 670 12

BsmFI GGGACnnnnnnnnnn'nnnn\_  
 Cuts at: 0 338 479 614 762 810 2080 2360  
 Size: 338 141 135 148 48 1270 280  
 Fragments arranged by size:  
 1270 338 280 148 141 135 48

FIG. 18D

Bsp24I GACnnnnnnTGGnnnnnnnnnnnn'  
 Cuts at: 0 52 84 239 271 569 601 2062 2094  
 Size: 52 32 155 32 298 32 1461 32  
 Cuts at: 2094 2360  
 Size: 266  
 Fragments arranged by size:  
 1461 298 266 155 52 32 32 32 32  
 Bsp1286I G\_dGCh'C  
 Cuts at: 0 56 105 508 714 1009 1521 1559 1592  
 Size: 56 49 403 206 295 512 38 33  
 Cuts at: 1592 1633 2109 2360  
 Size: 41 476 251  
 Fragments arranged by size:  
 512 476 403 295 251 206 56 49 41 38 33  
 BspMI ACCTGCnnnn'nnnn\_  
 Cuts at: 0 1194 2360  
 Size: 1194 1166  
 BsrI ACTG\_Gn'  
 Cuts at: 0 206 789 1154 1667 1979 2360  
 Size: 206 583 365 513 312 381  
 Fragments arranged by size:  
 583 513 381 365 312 206  
 BsrDI GCAATG\_nn'  
 Cuts at: 0 220 1646 2360  
 Size: 220 1426 714  
 Fragments arranged by size:  
 1426 714 220  
 BsrGI T'GTAC\_A  
 Cuts at: 0 1273 2360  
 Size: 1273 1087  
 BstXI CCAn\_nnnn'nTGG  
 Cuts at: 0 942 1161 1256 2360  
 Size: 942 219 95 1104  
 Fragments arranged by size:  
 1104 942 219 95  
 BstYI r'GATC\_y  
 Cuts at: 0 965 1575 1947 2360  
 Size: 965 610 372 413  
 Fragments arranged by size:  
 965 610 413 372

FIG. 18E

Bsu36I CC'TnA\_GG

Cuts at: 0 2142 2360

Size: 2142 218

CjeI ACnnnnnnTGGnnnnnn'nnnnnn\_

Cuts at: 0 79 188 266 563 618 2056 2360

Size: 79 109 78 297 55 1438 304

Fragments arranged by size:

1438 304 297 109 79 78 55

CviRI TG'CA

Cuts at: 0 103 184 404 558 1216 1281 1476 1525

Size: 103 81 220 154 658 65 195 49

Cuts at: 1525 1704 1730 2360

Size: 179 26 630

Fragments arranged by size:

658 630 220 195 179 154 103 81  
65 49 26

DdeI C'TnA\_G

Cuts at: 0 502 536 672 1684 1765 1828 2017 2142

Size: 502 34 136 1012 81 63 189 125

Cuts at: 2142 2188 2297 2360

Size: 46 109 63

Fragments arranged by size:

1012 502 189 136 125 109 81 63 63 46 34

DpnI GA'TC

Cuts at: 0 967 1348 1406 1577 1949 2360

Size: 967 381 58 171 372 411

Fragments arranged by size:

967 411 381 372 171 58

DraIII CAC\_nnn'GTG

Cuts at: 0 852 2020 2360

Size: 852 1168 340

Fragments arranged by size:

1168 852 340

DsaI C'CryG\_G

Cuts at: 0 358 1462 1492 1852 1870 2036 2360

Size: 358 1104 30 360 18 166 324

Fragments arranged by size:

1104 360 358 324 166 30 18

EaeI y'GGCC\_r

Cuts at: 0 74 523 2026 2360

Size: 74 449 1503 334

Fragments arranged by size:

1503 449 334 74

FIG. 18F

```

Earl CTCTTCn'nnn_
Cuts at: 0 152 1509 2216 2360
Size: 152 1357 707 144
Fragments arranged by size:
1357 707 152 144
EciI TCCGCC
Cuts at: 0 313 891 2360
Size: 313 578 1469
Fragments arranged by size:
1469 578 313
Eco57I CTGAAGnnnnnnnnnnnnnnnn nn'
Cuts at: 0 432 629 2269 2360
Size: 432 197 1640 91
Fragments arranged by size:
1640 432 197 91
EcoNI CCTnn'n_nnAGG
Cuts at: 0 1372 1905 2248 2360
Size: 1372 533 343 112
Fragments arranged by size:
1372 533 343 112
EcoOI109I rG'GnC_Cy
Cuts at: 0 52 53 725 824 2231 2360
Size: 52 1 672 99 1407 129
Fragments arranged by size:
1407 672 129 99 52 1
EcoRI G'AATT_C
Cuts at: 0 1 2136 2360
Size: 1 2135 224
Fragments arranged by size:
2135 224 1
EcoRV GAT'ATC
Cuts at: 0 1380 2360
Size: 1380 980
FauI CCCGCnnnn'nn_
Cuts at: 0 590 1099 2360
Size: 590 509 1261
Fragments arranged by size:
1261 590 509
FokI GGATGnnnnnnnnnn'nnnn_
Cuts at: 0 189 460 882 1044 1272 1895 2252 2360
Size: 189 271 422 162 228 623 357 108
Fragments arranged by size:
623 422 357 271 228 189 162 108

```

FIG. 18G

FspI TGC'GCA  
 Cuts at: 0 1143 2360  
 Size: 1143 1217  
 GdiII y'GGCC\_G  
 Cuts at: 0 74 2360  
 Size: 74 2286  
 HaeI wGG'CCw  
 Cuts at: 0 123 219 280 430 525 2028 2360  
 Size: 123 96 61 150 95 1503 332  
 Fragments arranged by size:  
 1503 332 150 123 96 95 61  
 HgiEI ACCnnnnnnGGT  
 Cuts at: 0 254 2360  
 Size: 254 2106  
 HhaI G\_CG'C  
 Cuts at: 0 1106 1144 1793 2360  
 Size: 1106 38 649 567  
 Fragments arranged by size:  
 1106 649 567 38  
 Hin4I GAbnnnnnvTC  
 Cuts at: 0 471 727 1573 1578 1580 2263 2360  
 Size: 471 256 846 5 2 683 97  
 Fragments arranged by size:  
 846 683 471 256 97 5 2  
 HinfI G'AnT\_C  
 Cuts at: 0 195 881 981 1020 1862 2032 2360  
 Size: 195 686 100 39 842 170 328  
 Fragments arranged by size:  
 842 686 328 195 170 100 39  
 HphI GGTGAnnnnnnn\_n'  
 Cuts at: 0 380 916 1626 2360  
 Size: 380 536 710 734  
 Fragments arranged by size:  
 734 710 536 380  
 MaeII A'CG\_T  
 Cuts at: 0 691 1699 2360  
 Size: 691 1008 661  
 Fragments arranged by size:  
 1008 691 661

FIG. 18H



MaeIII 'GTnAC\_  
 Cuts at: 0 245 760 922 1149 1181 1338 1718 1823  
 Size: 245 515 162 227 32 157 380 105  
 Cuts at: 1823 2360  
 Size: 537  
 Fragments arranged by size:  
 537 515 380 245 227 162 157 105 32  
 MboII GAAGAnnnnnnnn\_n'  
 Cuts at: 0 20 169 383 524 876 1496 2170 2173  
 Size: 20 149 214 141 352 620 674 3  
 Cuts at: 2173 2203 2360  
 Size: 30 157  
 Fragments arranged by size:  
 674 620 352 214 157 149 141 30 20 3  
 MmeI TCCrACnnnnnnnnnnnnnnnnnnnn\_nn'  
 Cuts at: 0 30 2360  
 Size: 30 2330  
 MscI TGG'CCA  
 Cuts at: 0 525 2028 2360  
 Size: 525 1503 332  
 Fragments arranged by size:  
 1503 525 332  
 MslI CAynn'nnrTG  
 Cuts at: 0 352 1461 2360  
 Size: 352 1109 899  
 Fragments arranged by size:  
 1109 899 352  
 MspI C'CG\_G  
 Cuts at: 0 553 821 1042 1097 1673 1959 2360  
 Size: 553 268 221 55 576 286 401  
 Fragments arranged by size:  
 576 553 401 286 268 221 55  
 MspAII CmG'CkG  
 Cuts at: 0 181 392 444 519 544 2360  
 Size: 181 211 52 75 25 1816  
 Fragments arranged by size:  
 1816 211 181 75 52 25  
 NciI CC's\_GG  
 Cuts at: 0 553 821 822 1097 1959 2360  
 Size: 553 268 1 275 862 401  
 Fragments arranged by size:  
 862 553 401 275 268 1

FIG. 18I

NcoI C'CATG\_G  
 Cuts at: 0 1492 1852 2036 2360  
 Size: 1492 360 184 324  
 Fragments arranged by size:  
 1492 360 324 184

NdeI CA'TA\_TG  
 Cuts at: 0 2051 2360  
 Size: 2051 309

NlaIII \_CATG'  
 Cuts at: 0 20 837 1253 1496 1762 1856 1869 2040  
 Size: 20 817 416 243 266 94 13 171  
 Cuts at: 2040 2360  
 Size: 320  
 Fragments arranged by size:  
 817 416 320 266 243 171 94 20 13

PstI GAGTCnnnn'n\_  
 Cuts at: 0 189 975 2026 2360  
 Size: 189 786 1051 334  
 Fragments arranged by size:  
 1051 786 334 189

Psp5II rG'GwC\_Cy  
 Cuts at: 0 725 824 2360  
 Size: 725 99 1536  
 Fragments arranged by size:  
 1536 725 99

PstI C\_TGCA'G  
 Cuts at: 0 1283 1478 2360  
 Size: 1283 195 882  
 Fragments arranged by size:  
 1283 882 195

PvuII CAG'CTG  
 Cuts at: 0 181 392 519 544 2360  
 Size: 181 211 127 25 1816  
 Fragments arranged by size:  
 1816 211 181 127 25

RsaI GT'AC  
 Cuts at: 0 642 1032 1275 2360  
 Size: 642 390 243 1085  
 Fragments arranged by size:  
 1085 642 390 243

FIG. 18J

SanDI GG'GwC\_CC  
 Cuts at: 0 824 2360  
 Size: 824 1536  
 SapI GCTCTTCn'nnn\_  
 Cuts at: 0 1509 2216 2360  
 Size: 1509 707 144  
 Fragments arranged by size:  
 1509 707 144  
 Sau3AI 'GATC\_  
 Cuts at: 0 965 1346 1404 1575 1947 2360  
 Size: 965 381 58 171 372 413  
 Fragments arranged by size:  
 965 413 381 372 171 58  
 SfaNI GCATCnnnnn'nnnn\_  
 Cuts at: 0 230 860 1225 1235 2360  
 Size: 230 630 365 10 1125  
 Fragments arranged by size:  
 1125 630 365 230 10  
 SfcI C'TryA\_G  
 Cuts at: 0 304 460 1279 1474 2360  
 Size: 304 156 819 195 886  
 Fragments arranged by size:  
 886 819 304 195 156  
 SmaI CCC'GGG  
 Cuts at: 0 822 2360  
 Size: 822 1538  
 Sse8647I AG'GwC\_CT  
 Cuts at: 0 725 2360  
 Size: 725 1635  
 SspI AAT'ATT  
 Cuts at: 0 1539 2061 2360  
 Size: 1539 522 299  
 Fragments arranged by size:  
 1539 522 299  
 SnuI AGG'CCT  
 Cuts at: 0 280 430 2360  
 Size: 280 150 1930  
 Fragments arranged by size:  
 1930 280 150  
 StyI C'CwwG\_G  
 Cuts at: 0 1034 1492 1852 2036 2234 2360  
 Size: 1034 458 360 184 198 126  
 Fragments arranged by size:  
 1034 458 360 198 184 126

FIG. 18K

TaqI T'CG\_A  
 Cuts at: 0 999 1804 2360  
 Size: 999 805 556  
 Fragments arranged by size:  
 999 805 556

TaqII GACCGAnnnnnnnnn\_nn'  
 Cuts at: 0 342 2360  
 Size: 342 2018

TauI GCsGC  
 Cuts at: 0 310 380 2360  
 Size: 310 70 1980  
 Fragments arranged by size:  
 1980 310 70

TfiI G'AwT\_C  
 Cuts at: 0 881 1020 1862 2360  
 Size: 881 139 842 498  
 Fragments arranged by size:  
 881 842 498 139

ThaI CG'CG  
 Cuts at: 0 1106 2360  
 Size: 1106 1254

TseI GCwGC  
 Cuts at: 0 182 383 517 1093 1140 1178 1794 1841  
 Size: 182 201 134 576 47 38 616 47  
 Cuts at: 1841 1914 2360  
 Size: 73 446  
 Fragments arranged by size:  
 616 576 446 201 182 134 73 47 38

Tsp45I 'GTsAC\_  
 Cuts at: 0 245 922 1181 1338 1718 1823 2360  
 Size: 245 677 259 157 380 105 537  
 Fragments arranged by size:  
 677 537 380 259 245 157 105

Tsp509I 'AATT\_  
 Cuts at: 0 1 485 930 1527 1932 2136 2280 2318  
 Size: 1 484 445 597 405 204 144 38  
 Cuts at: 2318 2360  
 Size: 42  
 Fragments arranged by size:  
 597 484 445 405 204 144 42 38

FIG. 18L

Tth111I GACn'n\_nGTC  
 Cuts at: 0 64 2360  
 Size: 64 2296  
 Tth111II CAARCAAnnnnnnnnnn\_nn'  
 Cuts at: 0 708 2360  
 Size: 708 1652  
 UbaCI wGTACw  
 Cuts at: 0 1275 2360  
 Size: 1275 1085  
 XcmI CCAnnnn\_n'nnnnTGG  
 Cuts at: 0 484 2360  
 Size: 484 1876

Enzymes that do cut and were not excluded:

AccI	AceIII	AhdI	AlwI	AlwNI
ApaI	ApaBI	ApaLI	ApoI	AvaI
AvaII	BanI	BanII	BbsI	BbvI
Bce83I	BceFI	BfaI	BfiI	BglI
BglII	BmgI	BpmI	Bpu10I	BsaWI
BsaXI	BsbI	BscGI	BseRI	BsgI
BsiEI	BsiHKA I	BsmI	BsmAI	BsmBI
BsmFI	Bsp24I	Bsp1286I	BspMI	BsrI
BsrDI	BsrGI	BstXI	BstYI	Bsu36I
CjeI	CviRI	DdeI	DpnI	DraIII
DsaI	EaeI	EarI	EciI	Eco57I
EcoNI	EcoO109I	EcoRI	EcoRV	FauI
FokI	FspI	GdiII	HaeI	HgiEII
HhaI	Hin4I	HinFI	HphI	MaeII
MaeIII	MboII	MmeI	MscI	MslI
MspI	MspA1I	NciI	NcoI	NdeI
NlaIII	PleI	Psp5II	PstI	PvuII
RsaI	SanDI	SapI	Sau3AI	SfaNI
SfcI	SmaI	Sse8647I	SspI	StuI
StyI	TaqI	TaqII	TauI	TfiI
ThaI	TseI	Tsp45I	Tsp509I	Tth111I
Tth111II	UbaCIXcmI			

Enzymes that do not cut:

AatII	AflII	AflIII	AscI	AvrII
BaeI	BamHI	BcgI	BcgI	BclI
BpII	Bpu1102I	BsaI	BsaAI	BsaBI
BsaHI	BspEI	BspGI	BspLU11I	BsrBI
BsrFI	BssHII	BssSI	Bst1107I	BstEII
Clal	DraI	DrdI	DrdII	EagI
Eco47III	FseI	HaeII	HgaI	HincII

FIG. 18M

HindIII	HpaI	KpnI	MluI	MseI
MunI	NarI	NgoAIV	NheI	NotI
NruI	NsiI	NspI	NspV	PacI
Pfl1108I	PflMI	PinAI	PmeI	PmlI
PshAI	Psp1406I	PvuI	RcaI	RleAI
RsrII	SacI	SacII	SalI	ScaI
SexAI	SfiI	SgfI	SgrAI	SnaBI
SpeI	SphI	SrfI	Sse8387I	SunI
Swal	VspI	XbaI	XhoI	XmnI

Enzymes excluded; MinCuts: 1

MaxCuts: 10

AciI	AluI	BccI	BsaJI	BsII
BsoFI	Cac8I	CjeI	CjePI	CjePI
CviJI	EcoRII	HaeIII	MnlI	MwoI
NlaIV	Sau96I	ScrFI	TspRI	

FIG. 18N

(Linear)MAPSORT of: piglac.gb\_om check: 9514 from:1 to :2259  
 LOCUS PIGLAC 2259 bp ss-mRNA MAM  
 DEFINITION Sus scrofa lactoferrin mRNA, complete cds.  
 ACCESSION M81327 M61828  
 KEYWORDS lactoferrin.  
 SOURCE Sus scrofa lactational mammary gland cDNA to mRNA.  
 ORGANISM Sus scrofa . . .  
 Mismatch: 0 MinCuts = 1 MaxCuts: 10  
 With 209 enzymes: \*

AceIII CAGCTCnnnnnnn'nnnn\_  
 Cuts at: 0 497 915 1092 1740 2239 2259  
 Size: 497 418 177 648 499 20

Fragments arranged by size:  
 648 499 497 418 177 20

AlwI GGATCnnnn'n\_  
 Cuts at: 0 965 1531 1544 2036 2259  
 Size: 965 566 13 492 223

Fragments arranged by size:  
 965 566 492 223 13

AlwNI CAG\_nnn'CTG  
 Cuts at: 0 219 1034 1148 1196 2259  
 Size: 219 815 114 48 1063

Fragments arranged by size:  
 1063 815 219 114 48

ApaLI G'TGCA\_C  
 Cuts at: 0 1549 2259  
 Size: 1549 710

ApoI r'AATT\_y  
 Cuts at: 0 495 1488 1497 2259  
 Size: 495 993 9 762

Fragments arranged by size:  
 993 762 495 9

AvaI C'yCGr\_G  
 Cuts at: 0 33 787 2259  
 Size: 33 754 1472

Fragments arranged by size:  
 1472 754 33

AvaII G'GwC\_C  
 Cuts at: 0 791 932 1095 2259  
 Size: 791 141 163 1164

Fragments arranged by size:  
 1164 791 163 141

FIG. 19A

BaeI ACnnnnGTAYC

Cuts at: 0 1614 2259

Size: 1614 645

BamHI G'GATC\_C

Cuts at: 0 1536 2259

Size: 1536 723

BanI G'GyrC\_C

Cuts at: 0 624 1265 1636 1770 2259

Size: 624 641 371 134 489

Fragments arranged by size:

641 624 489 371 134

BanII G\_rGCy'C

Cuts at: 0 475 2259

Size: 475 1784

BccI CCATC

Cuts at: 0 81 197 233 530 842 956 1025 1229

Size: 81 116 36 297 312 114 69 204

Cuts at: 1229 1769 2048 2259

Size: 540 279 211

Fragments arranged by size:

540 312 297 279 211 204 116 114 81 69 36

BceII ACGGCnnnnnnnnnn'n\_

Cuts at: 0 1060 1075 1333 2259

Size: 1060 15 258 926

Fragments arranged by size:

1060 926 258 15

BcgI CGAnnnnnnTGCnnnnnnnnnn\_nn'

Cuts at: 0 367 401 2259

Size: 367 34 1858

Fragments arranged by size:

1858 367 34

BfiI ACTGGG

Cuts at: 0 456 1823 2259

Size: 456 1367 436

Fragments arranged by size:

1367 456 436

BglI GCCn\_nnn'nGGC

Cuts at: 0 201 394 1768 2259

Size: 201 193 1374 491

Fragments arranged by size:

1374 491 201 193

FIG. 19B



BglII A'GATC\_T

Cuts at: 0 286 2259

Size: 286 1973

BmgI GkGCCC

Cuts at: 0 518 1592 2259

Size: 518 1074 667

Fragments arranged by size:

1074 667 518

BplI GAGnnnnnCTC

Cuts at: 0 171 2259

Size: 171 2088

BpmI CTGGAGnnnnnnnnnnnnnnnn'\_nn'

Cuts at: 0 462 2259

Size: 462 1797

Bpu10I CC'TnA\_GC

Cuts at: 0 469 2149 2259

Size: 469 1680 110

Fragments arranged by size:

1680 469 110

BsaI GGTCTCn'nnnn\_

Cuts at: 0 1531 1841 1941 2259

Size: 1531 310 100 318

Fragments arranged by size:

1531 318 310 100

BsaWI w'CCGG\_w

Cuts at: 0 621 1939 2116 2259

Size: 621 1318 177 143

Fragments arranged by size:

1318 621 177 143

BsbI CAACAC

Cuts at: 0 1332 1560 1696 1975 2259

Size: 1332 228 136 279 284

Fragments arranged by size:

1332 284 279 228 136

BscGI CCCGT

Cuts at: 0 294 1011 2166 2259

Size: 294 717 1155 93

Fragments arranged by size:

1155 717 294 93

BseRI GAGGAGnnnnnnnnnn'\_nn'

Cuts at: 0 1116 2151 2259

Size: 1116 1035 108

Fragments arranged by size:

1116 1035 108

FIG. 19C

FIG. 19D

BspGI CTGGAC  
 Cuts at: 0 1098 1190 2259  
 Size: 1098 92 1069  
 Fragments arranged by size:  
 1098 1069 92  
 BspMI ACCTGCnnnn'nnnn  
 Cuts at: 0 394 703 2259  
 Size: 394 309 1556  
 Fragments arranged by size:  
 1556 394 309  
 BsrI ACTG\_Gn'  
 Cuts at: 0 119 257 459 756 860 1822 2259  
 Size: 119 138 202 297 104 962 437  
 Fragments arranged by size:  
 962 437 297 202 138 119 104  
 BsrDI GCAATG\_nn'  
 Cuts at: 0 1571 2259  
 Size: 1571 688  
 BsrFI r'CCGG\_y  
 Cuts at: 0 272 442 1117 2259  
 Size: 272 170 675 1142  
 Fragments arranged by size:  
 1142 675 272 170  
 BssSI C'TCGT\_G  
 Cuts at: 0 2251 2259  
 Size: 2251 8  
 BstXI CCAn\_nnnn'nTGG  
 Cuts at: 0 909 2259  
 Size: 909 1350  
 BstYI r'GATC\_y  
 Cuts at: 0 286 970 1536 2259  
 Size: 286 684 566 723  
 Fragments arranged by size:  
 723 684 566 286  
 Bsu36I CC'TnA\_GG  
 Cuts at: 0 1035 2209 2259  
 Size: 1035 1174 50  
 Fragments arranged by size:  
 1174 1035 50  
 Cac8I GCn'nGC  
 Cuts at: 0 1069 1119 1250 1439 1461 1888 2133 2193  
 Size: 1069 50 131 189 22 427 245 60  
 Cuts at: 2193 2259  
 Size: 66  
 Fragments arranged by size:  
 1069 427 245 189 131 66 60 50 22

FIG. 19E

```

CjeI ACnnnnnnTGGnnnnnnn'nnnnnn_
Cuts at: 0 64 164 242 410 530 585 855 1526
Size: 64 100 78 168 120 55 270 671
Cuts at: 1526 2259
Size: 733
Fragments arranged by size:
733 671 270 168 120 100 78 64 55
CviRI TG'CA
Cuts at: 0 160 562 641 1156 1183 1322 1486 1551
Size: 160 402 79 515 27 139 164 65
Cuts at: 1551 2259
Size: 708
Fragments arranged by size:
708 515 402 164 160 139 79 65 27
DpnI GA'TC
Cuts at: 0 288 972 1538 2030 2259
Size: 288 684 566 492 229
Fragments arranged by size:
684 566 492 288 229
DraIII CAC_nnn'GTG
Cuts at: 0 1557 2259
Size: 1557 702
DrdI GACnn_nn'nnGTC
Cuts at: 0 1185 2259
Size: 1185 1074
DrdII GAACCA
Cuts at: 0 364 1285 2259
Size: 364 921 974
Fragments arranged by size:
974 921 364
DsaI C'CryG_G
Cuts at: 0 1090 1348 1453 2259
Size: 1090 258 105 806
Fragments arranged by size:
1090 806 258 105
EaeI y'GGCC_r
Cuts at: 0 270 490 2259
Size: 270 220 1769
Fragments arranged by size:
1769 270 220

```

FIG. 19F

EagI C'GGCC\_G  
Cuts at: 0 270 2259  
Size: 270 1989

EarI CTCTTCn'nnn\_  
Cuts at: 0 15 295 1711 2259  
Size: 15 280 1416 548  
Fragments arranged by size:  
1416 548 280 15

EcoNI CCTnn'n\_nnAGG  
Cuts at: 0 67 2208 2259  
Size: 67 2141 51  
Fragments arranged by size:  
2141 67 51

EcoO109I rG'GnC\_Cy  
Cuts at: 0 791 932 1031 2145 2259  
Size: 791 141 99 1114 114  
Fragments arranged by size:  
1114 791 141 114 99

EcoRI G'AATT\_C  
Cuts at: 0 1497 2259  
Size: 1497 762

FauI CCCGCnnnn'nn\_  
Cuts at: 0 26 1241 2086 2140 2259  
Size: 26 1215 845 54 119  
Fragments arranged by size:  
1215 845 119 54 26

FokI GGATGnnnnnnnnn'nnnn\_  
Cuts at: 0 1011 1239 1434 1671 2218 2259  
Size: 1011 228 195 237 547 41  
Fragments arranged by size:  
1011 547 237 228 195 41

FspI TGC'GCA  
Cuts at: 0 524 1110 2259  
Size: 524 586 1149  
Fragments arranged by size:  
1149 586 524

GdIII y'GGCC\_G  
Cuts at: 0 270 2259  
Size: 270 1989

HaeI wGG'CCw  
Cuts at: 0 397 492 1164 2259  
Size: 397 95 672 1095  
Fragments arranged by size:  
1095 672 397 95

FIG. 19G

HgiEI ACCnnnnnnGGT

Cuts at: 0 230 2259

Size: 230 2029

HhaI G<sub>-</sub>CG'C

Cuts at: 0 525 1064 1089 1111 2259

Size: 525 539 25 22 1148

Fragments arranged by size:

1148 539 525 25 22

Hin4I GAbnnnnnvTC

Cuts at: 0 83 171 1235 1541 1791 2259

Size: 83 88 1064 306 250 468

Fragments arranged by size:

1064 468 306 250 88 83

HincII GTy'rAC

Cuts at: 0 1469 2259

Size: 1469 790

HinfI G'AnT<sub>-</sub>C

Cuts at: 0 305 987 2173 2259

Size: 305 682 1186 86

Fragments arranged by size:

1186 682 305 86

HphI GGTGAnnnnnnn<sub>-</sub>n'

Cuts at: 0 1373 1797 2259

Size: 1373 424 462

Fragments arranged by size:

1373 462 424

MaeIII 'GTnAC<sub>-</sub>

Cuts at: 0 221 433 862 1617 1679 1784 1803 2039

Size: 221 212 429 755 62 105 19 236

Cuts at: 2039 2259

Size: 220

Fragments arranged by size:

755 429 236 221 220 212 105 62 19

MboII GAAGAnnnnnnn<sub>-</sub>n'

Cuts at: 0 2 151 312 353 491 980 1728 1912

Size: 2 149 161 41 138 489 748 184

Cuts at: 1912 2259

Size: 347

Fragments arranged by size:

748 489 347 184 161 149 138 41

2

FIG. 19H

MscI TGG'CCA

Cuts at: 0 492 2259

Size: 492 1767

MslI CAynn'nnrTG

Cuts at: 0 1422 1452 2259

Size: 1422 30 807

Fragments arranged by size:

1422 807 30

MspAII CmG'CkG

Cuts at: 0 282 557 1050 2181 2259

Size: 282 275 493 1131 78

Fragments arranged by size:

1131 493 282 275 78

MwoI GCnn\_nnn'nnGC

Cuts at: 0 201 210 394 470 810 1068 1135 1138

Size: 201 9 184 76 340 258 67 3

Cuts at: 1138 1650 1768 2259

Size: 512 118 491

Fragments arranged by size:

512 491 340 258 201 184 118 76 67 9 3

NciI CC's\_GG

Cuts at: 0 192 413 714 788 789 1534 1625 1920

Size: 192 221 301 74 1 745 91 295

Cuts at: 1920 2259

Size: 339

Fragments arranged by size:

745 339 301 295 221 192 91 74 1

NcoI C'CATG\_G

Cuts at: 0 1453 2259

Size: 1453 806

NgoAIV G'CCGG\_C

Cuts at: 0 1117 2259

Size: 1117 1142

NlaIII \_CATG'

Cuts at: 0 5 155 804 1457 1830 2105 2259

Size: 5 150 649 653 373 275 154

Fragments arranged by size:

653 649 373 275 154 150 5

FIG. 19I

PflMI CCA<sub>n</sub>nnn'nTGG  
 Cuts at: 0 1577 2259  
 Size: 1577 682  
 Psp5II rG'GwC\_Cy  
 Cuts at: 0 791 932 2259  
 Size: 791 141 1327  
 Fragments arranged by size:  
 1327 791 141  
 PstI C\_TGCA'G  
 Cuts at: 0 1158 2259  
 Size: 1158 1101  
 PvuII CAG'CTG  
 Cuts at: 0 557 2181 2259  
 Size: 557 1624 78  
 Fragments arranged by size:  
 1624 557 78  
 RcaI T'CATG\_A  
 Cuts at: 0 2101 2259  
 Size: 2101 158  
 RsaI GT'AC  
 Cuts at: 0 261 680 999 1014 2259  
 Size: 261 419 319 15 1245  
 Fragments arranged by size:  
 1245 419 319 261 15  
 SanDI GG'GwC\_CC  
 Cuts at: 0 791 2259  
 Size: 791 1468  
 SapI GCTCTTCn'nnn\_  
 Cuts at: 0 15 2259  
 Size: 15 2244  
 Sau3AI 'GATC\_  
 Cuts at: 0 286 970 1536 2028 2259  
 Size: 286 684 566 492 231  
 Fragments arranged by size:  
 684 566 492 286 231  
 SfaNI GCATCnnnnn'nnnn\_  
 Cuts at: 0 206 938 1192 1202 2259  
 Size: 206 732 254 10 1057  
 Fragments arranged by size:  
 1057 732 254 206 10  
 SfcI C'TryA\_G  
 Cuts at: 0 334 427 1154 2259  
 Size: 334 93 727 1105  
 Fragments arranged by size:  
 1105 727 334 93

FIG. 19J



SmaI CCC'GGG  
 Cuts at: 0 789 2259  
 Size: 789 1470  
 Sse8647I AG'GwC\_CT  
 Cuts at: 0 932 2259  
 Size: 932 1327  
 SspI AAT'ATT  
 Cuts at: 0 2022 2259  
 Size: 2022 237  
 StuI AGG'CCT  
 Cuts at: 0 397 2259  
 Size: 397 1862  
 StyI C'CwwG\_G  
 Cuts at: 0 398 1453 1997 2259  
 Size: 398 1055 544 262  
 Fragments arranged by size:  
 1055 544 398 262  
 TaqI T'CG\_A  
 Cuts at: 0 77 377 749 2259  
 Size: 77 300 372 1510  
 Fragments arranged by size:  
 1510 372 300 77  
 TauI GCsGC  
 Cuts at: 0 116 202 270 1065 2259  
 Size: 116 86 68 795 1194  
 Fragments arranged by size:  
 1194 795 116 86 68  
 TfiI G'AwT\_C  
 Cuts at: 0 305 987 2173 2259  
 Size: 305 682 1186 86  
 Fragments arranged by size:  
 1186 682 305 86  
 ThaI CG'CG  
 Cuts at: 0 201 1064 2259  
 Size: 201 863 1195  
 Fragments arranged by size:  
 1195 863 201  
 Tsp45I 'GTsAC\_  
 Cuts at: 0 221 862 1679 1784 1803 2039 2259  
 Size: 221 641 817 105 19 236 220  
 Fragments arranged by size:  
 817 641 236 221 220 105 19

FIG. 19K

Tsp509I 'AATT\_  
 Cuts at: 0 495 1488 1497 1731 2244 2259  
 Size: 495 993 9 234 513 15  
 Fragments arranged by size:  
 993 513 495 234 15 9

Tth111I GACn'n\_nGTC  
 Cuts at: 0 49 2259  
 Size: 49 2210

Tth111II CAACAnnnnnnnnnn\_nn'  
 Cuts at: 0 234 577 675 1452 1922 2259  
 Size: 234 343 98 777 470 337  
 Fragments arranged by size:  
 777 470 343 337 234 98

UbaCI wGTACw  
 Cuts at: 0 261 680 2259  
 Size: 261 419 1579  
 Fragments arranged by size:  
 1579 419 261

XcmI CCAnnnn\_n'nnnnTGG  
 Cuts at: 0 396 1829 2259  
 Size: 396 1433 430  
 Fragments arranged by size:  
 1433 430 396

XmnI GAAnn'nnTTC  
 Cuts at: 0 9 348 2259  
 Size: 9 339 1911  
 Fragments arranged by size:  
 1911 339 9

Enzymes that do cut and were not excluded:

AceIII	AlwI	AlwNI	ApaLI	ApoI	AvaI	AvaII	BaeI
BamHI	BanI	BanII	BccI	BceFI	BcgI	BfI	BglI
BglII	BmgI	BpII	BpmI	Bpu10I	BsaI	BsaWI	Bsbl
BscGI	BseRI	BsgI	BsiEI	BsiHKAII	BsII	BsmI	BsmAI
BsmFI	Bsp24I	Bsp1286I	BspGI	BspMI	BsrI	BsrDI	BsrFI
BssSI	BstXI	BstYI	Bsu36I	Cac8I	CjeI	CviRI	DpnI
DraIII	DrdI	DrdII	DsaI	EaeI	EagI	EarI	EcoNI
EcoO109I	EcoRI	FauI	FokI	FspI	GdiII	HaeI	HgiEII
HhaI	Hin4I	HincII	HinfI	HphI	MaeIII	MboII	MscI
MslII	MspAII	MwoI	NciI	NcoI	NgoAIV	NlaIII	PfiMI
Psp5II	PstI	PvuII	RcaI	RsaI	SanDI	SapI	Sau3AI
SfaNI	SfcI	SmaI	Sse8647I	SspI	StuI	StyI	TaqI
TauI	TfiI	ThaI	Tsp45I	Tsp509I	Tth111I	Tth111II	UbaCI
XcmI	XmnI						

FIG. 19L

Enzymes that do not cut:

AatII	AccI	AflII	AflIII	AhdI	ApaI	ApaBI	AscI
AvrII	BbsI	Bce83I	BclI	BfaI	Bpu1102I	BsaAI	BsaBI
BsaHI	BsaXI	BsmBI	BspEI	BspLU11I	BsrBI	BsrGI	BssHII
Bst1107I	BstEII	ClaI	DraI	EciI	Eco47III	Eco57I	EcoRV
FseI	HaeII	HgaI	HindIII	HpaI	KpnI	MaeII	MluI
MmeI	MseI	MunI	NarI	NdeI	NheI	NotI	NruI
NsiI	NspI	NspV	PacI	Pfl1108I	PinAI	PleI	PmeI
PmlI	PshAI	Psp1406I	PvuI	RleAI	RsrII	SacI	SacII
Sall	ScaI	SexAI	SfiI	SgfI	SgrAI	SnaBI	SpeI
SphI	SrfI	Sse8387I	SunI	Swal	TaqII	TaqII	VspI
XbaI	XhoI						

Enzymes excluded; MinCuts: 1 MaxCuts: 10

AcII	AluI	BbvI	BsaII	BsoFI	CjeI	CjePI	CjePI
CviII	DdeI	EcoRII	HaeIII	MnlI	MspI	NlaIV	Sau96I
ScrFI	TseI	TspRI					

FIG. 19M

(Linear) MAPSORT of: bovlactof.gb\_om check: 2217 from: 1 to: 2351  
 LOCUS BOVLACTOF 2351 bp ss-mRNA MAM  
 DEFINITION Bovine lactoferrin mRNA, complete cds.  
 ACCESSION M63502  
 KEYWORDS lactoferrin.  
 SOURCE B.taurus, cDNA to mRNA.  
 ORGANISM Bos taurus . . .  
 Mismatch: 0 MinCuts = 1 MaxCuts: 10  
 With 209 enzymes: \*

AceIII CAGCTCnnnnnnn'nnnn\_  
 Cuts at: 0 494 526 969 1553 1841 2216 2351  
 Size: 494 32 443 584 288 375 135  
 Fragments arranged by size:  
 584 494 443 375 288 135 32

AflIII A'CryG\_T  
 Cuts at: 0 1913 2351  
 Size: 1913 438

AhdI GACnn\_n'nnGTC  
 Cuts at: 0 1460 2351  
 Size: 1460 891

AlwI GGATCnnnn'n\_  
 Cuts at: 0 480 1019 1032 2351  
 Size: 480 539 13 1319  
 Fragments arranged by size:  
 1319 539 480 13

AlwNI CAG\_nnn'CTG  
 Cuts at: 0 1600 1631 1928 1946 2351  
 Size: 1600 31 297 18 405  
 Fragments arranged by size:  
 1600 405 297 31 18

ApoI r'AATT\_y  
 Cuts at: 0 549 1442 1551 2351  
 Size: 549 893 109 800  
 Fragments arranged by size:  
 893 800 549 109

AvaI C'yCGr\_G  
 Cuts at: 0 101 522 652 2351  
 Size: 101 421 130 1699  
 Fragments arranged by size:  
 1699 421 130 101

FIG. 20A

AvaII G'GwC\_C  
Cuts at: 0 305 416 460 770 845 986 1149 2244  
Size: 305 111 44 310 75 141 163 1095  
Cuts at: 2244 2351  
Size: 107  
Fragments arranged by size:  
1095 310 305 163 141 111 107 75 44

BamHI G'GATC\_C  
Cuts at: 0 1024 2351  
Size: 1024 1327

BanI G'GyrC\_C  
Cuts at: 0 678 806 1319 1393 1690 1824 2351  
Size: 678 128 513 74 297 134 527  
Fragments arranged by size:  
678 527 513 297 134 128 74

BanII G\_rGCy'C  
Cuts at: 0 80 529 1062 1435 2351  
Size: 80 449 533 373 916  
Fragments arranged by size:  
916 533 449 373 80

BbsI GAAGACnn'nnnn\_  
Cuts at: 0 895 2351  
Size: 895 1456

BbvI GCAGCnnnnnnnn'nnnn\_  
Cuts at: 0 83 342 409 412 1842 1915 1920 2351  
Size: 83 259 67 3 1430 73 5 431  
Fragments arranged by size:  
1430 431 259 83 73 67 5 3

BccI CCATC  
Cuts at: 0 120 128 162 278 881 1283 1823 2351  
Size: 120 8 34 116 603 402 540 528  
Fragments arranged by size:  
603 540 528 402 120 116 34 8

Bce83I CTTGAGnnnnnnnnnnnnnn'\_nn'  
Cuts at: 0 524 2351  
Size: 524 1827

BceII ACGGCnnnnnnnnnnnn'n\_  
Cuts at: 0 370 1129 1231 1387 1462 2113 2351  
Size: 370 759 102 156 75 651 238  
Fragments arranged by size:  
759 651 370 238 156 102 75

BfaI C'TA\_G  
Cuts at: 0 1365 2183 2351  
Size: 1365 818 168  
Fragments arranged by size:  
1365 818 168

FIG. 20B

BfiI ACTGGG  
 Cuts at: 0 1776 2351  
 Size: 1776 575  
 BglI GCCn\_nnn'nGGC  
 Cuts at: 0 448 1578 1822 2351  
 Size: 448 1130 244 529  
 Fragments arranged by size:  
 1130 529 448 244  
 BglII A'GATC\_T  
 Cuts at: 0 337 2351  
 Size: 337 2014  
 BmgI GkGCCC  
 Cuts at: 0 1572 1646 2351  
 Size: 1572 74 705  
 Fragments arranged by size:  
 1572 705 74  
 BpmI CTGGAGnnnnnnnnnnnnnnn\_nn'  
 Cuts at: 0 516 727 2216 2351  
 Size: 516 211 1489 135  
 Fragments arranged by size:  
 1489 516 211 135  
 Bpu10I CC'TnA\_GC  
 Cuts at: 0 1699 2202 2351  
 Size: 1699 503 149  
 Fragments arranged by size:  
 1699 503 149  
 BsaI GGTCTCn'nnnn\_  
 Cuts at: 0 1373 2351  
 Size: 1373 978  
 BsaAI yAC'GTr  
 Cuts at: 0 1916 2351  
 Size: 1916 435  
 BsaHI Gr'CG\_yC  
 Cuts at: 0 32 807 1218 2351  
 Size: 32 775 411 1133  
 Fragments arranged by size:  
 1133 775 411 32  
 BsaWI w'CCGG\_w  
 Cuts at: 0 15 1339 2351  
 Size: 15 1324 1012  
 Fragments arranged by size:  
 1324 1012 15  
 BsaXI ACnnnnnCTCC  
 Cuts at: 0 634 1058 2351  
 Size: 634 424 1293  
 Fragments arranged by size:  
 1293 634 424

FIG. 20C

BsbI CAACAC

Cuts at: 0 2029 2351

Size: 2029 322

BscGI CCCGT

Cuts at: 0 449 498 702 2351

Size: 449 49 204 1649

Fragments arranged by size:

1649 449 204 49

BseRI GAGGAGnnnnnnnn\_nn'

Cuts at: 0 638 1119 1170 2198 2351

Size: 638 481 51 1028 153

Fragments arranged by size:

1028 638 481 153 51

BsiHKA I G\_wGCw'C

Cuts at: 0 191 1767 2351

Size: 191 1576 584

Fragments arranged by size:

1576 584 191

BsmAI GTCTCn'nnnn\_

Cuts at: 0 361 703 723 949 1373 1897 2351

Size: 361 342 20 226 424 524 454

Fragments arranged by size:

524 454 424 361 342 226 20

BsmBI CGTCTCn'nnnn\_

Cuts at: 0 703 723 2351

Size: 703 20 1628

Fragments arranged by size:

1628 703 20

BsoFI GC'n\_GC

Cuts at: 0 97 155 321 331 401 423 1193 1856

Size: 97 58 166 10 70 22 770 663

Cuts at: 1856 1909 1929 2351

Size: 53 20 422

Fragments arranged by size:

770 663 422 166 97 70 58 53 22 20 10

Bsp24I GACnnnnnnTGnnnnnnnn\_nnnnn'

Cuts at: 0 76 108 260 292 590 622 882 914

Size: 76 32 152 32 298 32 260 32

Cuts at: 914 1725 1757 2351

Size: 811 32 594

Fragments arranged by size:

811 594 298 260 152 76 32 32 32 32 32

FIG. 20D

Bsp1286I G\_dGCh'C  
 Cuts at: 0 80 191 529 1062 1435 1574 1648 1767  
 Size: 80 111 338 533 373 139 74 119  
 Cuts at: 1767 2351  
 Size: 584  
 Fragments arranged by size:  
 584 533 373 338 139 119 111 80 74  
 BspEI T'CCGG\_A  
 Cuts at: 0 15 2351  
 Size: 15 2336  
 BspGI CTGGAC  
 Cuts at: 0 416 511 1634 2351  
 Size: 416 95 1123 717  
 Fragments arranged by size:  
 1123 717 416 95  
 BspMI ACCTGCnnnn'nnnn\_  
 Cuts at: 0 448 997 2351  
 Size: 448 549 1354  
 Fragments arranged by size:  
 1354 549 448  
 BsrI ACTG\_Gn'  
 Cuts at: 0 324 635 773 810 1779 2351  
 Size: 324 311 138 37 969 572  
 Fragments arranged by size:  
 969 572 324 311 138 37  
 BsrBI GAG'CGG  
 Cuts at: 0 1192 2351  
 Size: 1192 1159  
 BsrDI GCAATG\_nn'  
 Cuts at: 0 2101 2351  
 Size: 2101 250  
 BstXI CCA\_nnnn'nTGG  
 Cuts at: 0 963 2351  
 Size: 963 1388  
 BstYI r'GATC\_y  
 Cuts at: 0 337 1024 2351  
 Size: 337 687 1327  
 Fragments arranged by size:  
 1327 687 337  
 Bsu36I CC'TnA\_GG  
 Cuts at: 0 1089 1153 2351  
 Size: 1089 64 1198  
 Fragments arranged by size:  
 1198 1089 64

FIG. 20E



CviRI TG'CA

Cuts at: 0 425 577 616 695 1237 1491 1770 2174

Size: 425 152 39 79 542 254 279 404

Cuts at: 2174 2351

Size: 177

Fragments arranged by size:

542 425 404 279 254 177 152 79 39

DpnI GA'TC

Cuts at: 0 339 474 897 1026 1518 2351

Size: 339 135 423 129 492 833

Fragments arranged by size:

833 492 423 339 135 129

DraIII CAC\_nnn'GTG

Cuts at: 0 1886 2035 2351

Size: 1886 149 316

Fragments arranged by size:

1886 316 149

DrdI GACnn\_nn'nnGTC

Cuts at: 0 353 1239 2351

Size: 353 886 1112

Fragments arranged by size:

1112 886 353

DrdII GAACCA

Cuts at: 0 146 634 659 2351

Size: 146 488 25 1692

Fragments arranged by size:

1692 488 146 25

DsaI C'CryG\_G

Cuts at: 0 1144 1213 1402 1477 1507 2351

Size: 1144 69 189 75 30 844

Fragments arranged by size:

1144 844 189 75 69 30

EaeI y'GGCC\_r

Cuts at: 0 321 382 977 1193 2041 2098 2351

Size: 321 61 595 216 848 57 253

Fragments arranged by size:

848 595 321 253 216 61 57

FIG. 20F

FIG. 20G

FspI TGC'GCA

Cuts at: 0 1541 2351

Size: 1541 810

GdiII y'GGCC\_G

Cuts at: 0 321 382 977 1193 2098 2351

Size: 321 61 595 216 905 253

Fragments arranged by size:

905 595 321 253 216 61

HaeI wGG'CCw

Cuts at: 0 1315 2043 2351

Size: 1315 728 308

Fragments arranged by size:

1315 728 308

HaeII r\_GCGC'y

Cuts at: 0 810 1050 2351

Size: 810 240 1301

Fragments arranged by size:

1301 810 240

HgaI GACGCnnnnn'nnnnn

Cuts at: 0 40 1207 2351

Size: 40 1167 1144

Fragments arranged by size:

1167 1144 40

HgiEII ACCnnnnnnGGT

Cuts at: 0 275 2351

Size: 275 2076

HhaI G\_CG'C

Cuts at: 0 809 920 1049 1118 1542 2151 2239 2351

Size: 809 111 129 69 424 609 88 112

Fragments arranged by size:

809 609 424 129 112 111 88 69

Hin4I GAbnnnnnvTC

Cuts at: 0 1289 1459 1588 1845 2351

Size: 1289 170 129 257 506

Fragments arranged by size:

1289 506 257 170 129

HincII GTy'rAC

Cuts at: 0 609 1523 2351

Size: 609 914 828

Fragments arranged by size:

914 828 609

FIG. 20H

HindIII A'AGCT\_T  
 Cuts at: 0 903 2351  
 Size: 903 1448

HinfI G'AnT\_C  
 Cuts at: 0 19 354 487 516 1002 1041 1597 1790  
 Size: 19 335 133 29 486 39 556 193  
 Cuts at: 1790 1877 2351  
 Size: 87 474  
 Fragments arranged by size:  
 556 486 474 335 193 133 87 39 29 19

HphI GGTGAnnnnnnn\_n'  
 Cuts at: 0 191 1121 2351  
 Size: 191 930 1230  
 Fragments arranged by size:  
 1230 930 191

KpnI G\_GTAC'C  
 Cuts at: 0 1397 2351  
 Size: 1397 954

MaeII A'CG\_T  
 Cuts at: 0 112 712 1201 1705 1714 1915 2064 2351  
 Size: 112 600 489 504 9 201 149 287  
 Fragments arranged by size:  
 600 504 489 287 201 149 112 9

MaeIII 'GTnAC\_  
 Cuts at: 0 266 517 1202 1838 2093 2351  
 Size: 266 251 685 636 255 258  
 Fragments arranged by size:  
 685 636 266 258 255 251

MboII GAAGAnnnnnnn\_n'  
 Cuts at: 0 41 188 404 545 900 1094 1175 2082  
 Size: 41 147 216 141 355 194 81 907  
 Cuts at: 2082 2351  
 Size: 269  
 Fragments arranged by size:  
 907 355 269 216 194 147 141 81 41

FIG. 20I

MmeI TCCrACnnnnnnnnnnnnnnnnnnnnnn\_nn'

Cuts at: 0 2248 2351

Size: 2248 103

MscI TGG'CCA

Cuts at: 0 2043 2351

Size: 2043 308

MseI T'TA\_A

Cuts at: 0 724 2351

Size: 724 1627

MslI CAynn'nnrTG

Cuts at: 0 204 373 480 1476 1506 2351

Size: 204 169 107 996 30 845

Fragments arranged by size:

996 845 204 169 107 30

MspI C'CG\_G

Cuts at: 0 16 237 302 431 653 976 1340 1678

Size: 16 221 65 129 222 323 364 338

Cuts at: 1678 1974 2351

Size: 296 377

Fragments arranged by size:

377 364 338 323 296 222 221 129 65 16

MspAII CmG'CkG

Cuts at: 0 413 422 465 565 2351

Size: 413 9 43 100 1786

Fragments arranged by size:

1786 413 100 43 9

NarI GG'CG\_CC

Cuts at: 0 807 2351

Size: 807 1544

NciI CC's\_GG

Cuts at: 0 238 303 653 654 976 1679 1974 2351

Size: 238 65 350 1 322 703 295 377

Fragments arranged by size:

703 377 350 322 295 238 65 1

NcoI C'CATG\_G

Cuts at: 0 1507 2351

Size: 1507 844

NheI G'CTAG\_C

Cuts at: 0 2182 2351

Size: 2182 169

NlaIII \_CATG'

Cuts at: 0 44 287 858 1441 1511 2351

Size: 44 243 571 583 70 840

Fragments arranged by size:

840 583 571 243 70 44

FIG. 20J

PflMI CCA<sub>n</sub>nnn'nTGG  
 Cuts at: 0 1631 2351  
 Size: 1631 720

PleI GAGTCnnnn'n  
 Cuts at: 0 27 362 524 996 1591 2351  
 Size: 27 335 162 472 595 760  
 Fragments arranged by size:  
 760 595 472 335 162 27

PmlI CAC'GTG  
 Cuts at: 0 1916 2351  
 Size: 1916 435

Psp5II rG'GwC\_Cy  
 Cuts at: 0 305 845 986 1149 2244 2351  
 Size: 305 540 141 163 1095 107  
 Fragments arranged by size:  
 1095 540 305 163 141 107

Psp1406I AA'CG\_TT  
 Cuts at: 0 112 2351  
 Size: 112 2239

PstI C\_TGCA'G  
 Cuts at: 0 697 1493 1772 2351  
 Size: 697 796 279 579  
 Fragments arranged by size:  
 796 697 579 279

PvuII CAG'CTG  
 Cuts at: 0 413 422 565 2351  
 Size: 413 9 143 1786  
 Fragments arranged by size:  
 1786 413 143 9

RsaI GT'AC  
 Cuts at: 0 125 501 1053 1122 1395 1665 2351  
 Size: 125 376 552 69 273 270 686  
 Fragments arranged by size:  
 686 552 376 273 270 125 69

SanDI GG'GwC\_CC  
 Cuts at: 0 305 2351  
 Size: 305 2046

SapI GCTCTTCn'nnn\_  
 Cuts at: 0 54 2351  
 Size: 54 2297

Sau3AI 'GATC\_  
 Cuts at: 0 337 472 895 1024 1516 2351  
 Size: 337 135 423 129 492 835  
 Fragments arranged by size:  
 835 492 423 337 135 129

FIG. 20K

ScaI AGT'ACT

Cuts at: 0 1665 2351

Size: 1665 686

SfaNI GCATCnnnnn'nnnn

Cuts at: 0 250 251 806 1246 1256 2351

Size: 250 1 555 440 10 1095

Fragments arranged by size:

1095 555 440 250 10 1

SfiI C'TryA\_G

Cuts at: 0 693 1489 1768 2351

Size: 693 796 279 583

Fragments arranged by size:

796 693 583 279

SmaI CCC'GGG

Cuts at: 0 654 2351

Size: 654 1697

SspI AAT'ATT

Cuts at: 0 2076 2351

Size: 2076 275

StyI C'CwwG\_G

Cuts at: 0 71 80 223 452 1507 2351

Size: 71 9 143 229 1055 844

Fragments arranged by size:

1055 844 229 143 71 9

TaqI T'CG\_A

Cuts at: 0 116 523 1032 1819 2351

Size: 116 407 509 787 532

Fragments arranged by size:

787 532 509 407 116

TaqII GACCGAnnnnnnnnn'nn'

Cuts at: 0 174 457 2351

Size: 174 283 1894

Fragments arranged by size:

1894 283 174

TauI GCsGC

Cuts at: 0 155 321 1193 2351

Size: 155 166 872 1158

Fragments arranged by size:

1158 872 166 155

TfiI G'AwT\_C

Cuts at: 0 487 1041 1790 1877 2351

Size: 487 554 749 87 474

Fragments arranged by size:

749 554 487 474 87

FIG. 20L

ThaI CG'CG

Cuts at: 0 246 1118 2239 2351

Size: 246 872 1121 112

Fragments arranged by size:

1121 872 246 112

TseI GCwGC

Cuts at: 0 97 331 401 423 1856 1909 1929 2351

Size: 97 234 70 22 1433 53 20 422

Fragments arranged by size:

1433 422 234 97 70 53 22 20

Tsp45I 'GTsAC\_

Cuts at: 0 266 517 1202 1838 2093 2351

Size: 266 251 685 636 255 258

Fragments arranged by size:

685 636 266 258 255 251

Tsp509I 'AATT\_

Cuts at: 0 549 1442 1551 2298 2329 2351

Size: 549 893 109 747 31 22

Fragments arranged by size:

893 747 549 109 31 22

TspRI CAGTGnn'

Cuts at: 0 171 642 742 817 1182 1232 1304 1772

Size: 171 471 100 75 365 50 72 468

Cuts at: 1772 2036 2351

Size: 264 315

Fragments arranged by size:

471 468 365 315 264 171 100 75 72 50

Tth111I GACn'n\_nGTC

Cuts at: 0 88 515 1737 2351

Size: 88 427 1222 614

Fragments arranged by size:

1222 614 427 88

Tth111I CAARCAnnnnnnnnnn\_nn'

Cuts at: 0 279 604 729 1368 1938 1976 2351

Size: 279 325 125 639 570 38 375

Fragments arranged by size:

639 570 375 325 279 125 38

FIG. 20M



UbaCI wGTACw

Cuts at: 0 1665 2351

Size: 1665 686

XcmI CCAnnnn\_n'nnnnTGG

Cuts at: 0 450 2351

Size: 450 1901

XhoI C'TCGA\_G

Cuts at: 0 522 2351

Size: 522 1829

XmnI GAAnn'nnTTC

Cuts at: 0 48 232 2351

Size: 48 184 2119

Fragments arranged by size:

2119 184 48

Enzymes that do cut and were not excluded:

AceIII	AflIII	AhdI	AlwI	AlwNI	ApoI	AvaI	AvaII
BamHI	BanI	BanII	BbsI	BbvI	BccI	Bce83I	BceII
BfaI	BfiI	BglI	BglII	BmgI	BpmI	Bpu10I	BsaI
BsaAI	BsaHI	BsaWI	BsaXI	BsbI	BscGI	BseRI	BsiHKAII
BsmAI	BsmBI	BsoFI	Bsp24I	Bsp1286I	BspEI	BspGI*	BspMI
BsrI	BsrBI	BsrDI	BstXI	BstYI	Bsu36I	CviRI	DpnI
DraIII	DrdI	DrdII	DsaI	EaeI	EarI	EciI	Eco57I
EcoNI	EcoO109I	EcoRI	FauI	FokI	FspI	GdiII	HaeI
HaeII	HgaI	Hgi	EII	HhaI	Hin4I	HincII	HindIII
HinfI	HphI	KpnI	MaeII	MaeIII	MboII	MmeI	MscI
MseI	MslI	MspI	MspAII	NarI	NciI	NcoI	NheI
NlaIII	PflMI	PleI	PmlI	Psp5II	Psp1406I	PstI	PvuII
RsaI	SanDI	SapI	Sau3AI	ScaI	SfaNI	SfcI	SmaI
SspI	StyI	TaqI	TaqII	TauI	TfiI	ThaI	TseI
Tsp45I	Tsp509I	TspRI	Tth111I	Tth111II	UbaCI	XcmI	XhoI

XmnI

Enzymes that do not cut:

AatII	AccI	AflII	ApaI	ApaBI	ApalI	AscI	AvrII
BaeI	BcgI	BcgI	BclI	BpII	Bpu1102I	BsaBI	BsgI
BsiEI	BsmI	BspLU11I	BsrFI	BsrGI	BssHII	BssSI	Bst1107I
BstEII	Clal	DraI	EagI	Eco47III	EcoRV	FseI	HpaI
MluI	MunI	NdeI	NgoAIV	NotI	NruI	NsiI	NspI
NspV	PacI	Pfl1108I	PinAI	PmeI	PshAI	PvuI	RcaI
RleAI	RsrII	SacI	SacII	Sall	SexAI	Sfil	SgfI
SgrAI	SnaBI	SpeI	SphI	SrfI	Sse8387I	Sse8647I	StuI
SunI	SwaI	VspI	XbaI				

Enzymes excluded; MinCuts: 1 MaxCuts: 10

AcII	AluI	BsaII	BslI	BsmFI	Cac8I	CjeI	CjeI
CjePI	CjePI	CviII	DdeI	EcoRII	HaeIII	MnII	MwoI
NlaIV	Sau96I	ScrFI					

FIG. 20N